

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 15:27:15 ; Search time 17 Seconds

CY (without alignments)
1421.866 Million cell updates/sec

Title: NP418220

Perfect score: 2633
Sequence: 1 MADSQLSGAPEGAEYLRAY.....LGYDCHDETNNPAERFLAG 514

Scoring table: BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2633	100.0	514	1	THD1_ECOLI
2	2525	95.9	514	1	THD1_SALTY
3	1857.5	70.5	513	1	THD1_PASNU
4	1738.5	66.0	513	1	THD1_HAEIN
5	1383	52.5	507	1	THD1_BURCE
6	1212.5	46.1	576	1	THDH_YEAST
7	1136	43.1	550	1	THDH_ARXAD
8	1087	41.3	592	1	THD1_ARATH
9	994.5	37.8	595	1	THD1_LYCES
10	937.5	35.6	590	1	THD1_CICAR
11	642	24.4	359	1	THD1_SOLRU
12	642	24.4	422	1	THD1_BACSU
13	608	23.1	415	1	THD1_BACHD
14	600	22.8	416	1	THD1_LACLA
15	578.5	22.0	429	1	THD1_MYCTU
16	577	21.9	427	1	THD1_MYCLE
17	566	21.5	436	1	THD1_CORGL
18	534	20.3	329	1	THD2_SALTY
19	529	20.1	329	1	THD2_ECOLI
20	485	18.4	326	1	YKVB_YEAST
21	470	17.9	323	1	YKNE_YEAST
22	466	17.7	332	1	YATJ_RHIN
23	378	14.4	339	1	SRR_MOUSE
24	357	13.6	340	1	SRR_HUMAN
25	308	11.7	328	1	SDHL_HUMAN
26	279	10.6	362	1	SDHL_RAT
27	233.5	8.8	307	1	CYSK_FIASP
28	230	8.7	307	1	CYSK_BACSU
29	228.5	8.7	360	1	SDHL_YEAST
30	225.5	8.6	360	1	STDH_YEAST
31	221.5	8.4	405	1	THRC_METUA
32	215.5	8.2	352	1	THRC_BACSP
33	211.5	8.0	404	1	DPAL_SALTY

34	209.5	8.0	352	1	THRC_BACSU	P04990 bacillus su
35	208	7.9	354	1	THRC_BACHD	Q9K763 bacillus ha
36	208	7.9	398	1	DPAL_ECOLI	Q46804 escherichia
37	194.5	7.4	310	1	CYSK_MYCTU	P95230 mycobacteri
38	186	7.1	311	1	CYSK_BACSU	O34476 bacillus su
39	186	7.1	325	1	CYK2_ORYSA	Q34468 oryza sativ
40	183.5	7.0	299	1	CYSM_CAMGE	P71128 campylobact
41	177.5	6.7	310	1	CYSK_MYCLE	O32978 mycobacteri
42	176.5	6.7	392	1	CYSL_ARATH	P47999 arabidopsis
43	174	6.6	325	1	CYSK_SPIOL	O00834 spiniacia ol
44	173.5	6.6	325	1	CYSK_WHEAT	P38076 triticum ae
45	172	6.5	382	1	THRC_SINY3	P74193 synechocyst

ALIGNMENTS

RESULT 1	THD1_ECOLI	STANDARD;	PRT;	514 AA.
ID	THD1_ECOLI			
AC	P04968;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine deaminase).			
GN	ILVA OR B3772.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=86056322; PubMed=3315862;			
RA	Cox J.L., Cox B.J., Fidanza V., Calhoun D.H.,			
RT	"The complete nucleotide sequence of the livGMEBA cluster of			
RT	Escherichia coli K-12."			
RL	Gene 56:185-198(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Garrison E., Harms E., Umbarger H.E.,			
RT	Submitted (AUG-1986) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=87174741; PubMed=3550695;			
RA	Lawcher R.P., Wek R.C., Lopes J.M., Pereira R., Tailon B.E.,			
RT	Hatfield G.W.;			
RT	"The complete nucleotide sequence of the livGMEBA operon of			
RT	Escherichia coli K-12."			
RL	Nucleic Acids Res. 15:2137-2155(1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=92358234; PubMed=1379743;			
RA	Daniels D.L., Plunkett G., III, Burland V.D., Blattner F.R.,			
RT	"Analysis of the Escherichia coli genome: DNA sequence of the region			
RT	from 84.5 to 86.5 minutes."			
RL	Science 257:771-778(1992).			
RN	[5]			
RP	SEQUENCE OF 439-514 FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=86111952; PubMed=3003115;			
RA	Wek R.C., Hatfield G.W.;			
RT	"Nucleotide sequence and in vivo expression of the livY and livC			
RT	genes in Escherichia coli K12. Transcription from divergent			
RT	overlapping promoters."			
RL	J. Biol. Chem. 261:2441-2450(1986).			
RN	[6]			
RP	SEQUENCE OF 1-10 FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=89326124; PubMed=2473940;			

RA Lopes J.M., Lawther R.P.;
RT "Physical identification of an internal promoter, ilvP, in the
RT distal portion of the ilvGMEDA operon."; <http://www.ncbi.nlm.nih.gov/PMOBS/summary/summary.html?acc=U00001>
RL Gene 76:255-269(1989).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=98230745; PubMed=9562556;
RA Gallagher D.T., Gilliland G.L., Xiao G., Zondlo J., Fisher K.E.,
RA Chinchilla D., Eisenstein E.;
RT "Structure and control of pyridoxal phosphate dependent allosteric
RT threonine deaminase.";
RL Structure 6:465-475(1998).
CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydration
CC of threonine, followed by rehydration and liberation of ammonia.
CC Deaminates L-threonine, but also L-serine to a lesser extent.
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHEREAS
CC VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
CC -1- PATHWAY: Isoleucine biosynthesis; first step.
CC -1- SUBUNIT: Homotetramer.
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC -----
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CC -----
DR EMBL: X04890; CAA28577.1; -;
DR EMBL: K03503; AAA24014.1; -;
DR EMBL: M10313; AAB59054.1; -;
DR EMBL: M11689; AAA24027.1; -;
DR EMBL: M32253; AAA24024.1; -;
DR EMBL: M87049; AAA67575.1; -;
DR EMBL: AB000453; AAC7492.1; -;
DR EMBL: M25497; AAA24015.1; -;
DR PIR: B27310; DMECTS.
DR PDB: 1TDJ; 18-NOV-98.
DR ECO2DBASE; F050.1; 6TH EDITION.
DR EcoGene; EG10493; ilvA.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR000634; S/T dehydratase.
DR InterPro; IPR005787; Thz dehydratase.
DR InterPro; IPR001721; ThzDh_C.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thz dehydratase.
DR TIGRFAMs; TIGR01124; ilvA_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
DR Isoleucine biosynthesis; lyase; pyridoxal phosphate;
KW Allosteric enzyme; 3D-structure; Complete proteome.
FT BLINDING 62 62
FT FTBLINDING 120 120 A -> R (IN REF. 2).
FT FTBLINDING 140 140 A -> R (IN REF. 2).
FT FTBLINDING 195 195 G -> C (IN REF. 2).
FT FTBLINDING 243 243 A -> G (IN REF. 3).
FT FTBLINDING 334 334 G -> V (IN REF. 2).
FT FTBLINDING 6 7
FT FTBLINDING 13 22
FT FTBLINDING 25 27
FT FTBLINDING 28 28
FT STRAND 34 36
FT STRAND 38 43
FT STRAND 44 45
FT STRAND 47 51
FT STRAND 53 55
FT STRAND 57 58
FT STRAND 62 62
FT STRAND 63 71
FT STRAND 72 75

FT STRAND 83 86
FT STRAND 91 100
FT STRAND 101 102
FT STRAND 105 108
FT STRAND 115 124
FT STRAND 127 129
FT STRAND 135 149
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FT STRAND 462 464
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FT STRAND 470 470
FT STRAND 475 479
FT STRAND 498 504
FT STRAND 503 504
FT STRAND 506 511
FT STRAND 512 512
SQ SEQUENCE 514 AA; 56195 MW; 9D389A0EDB08DE92 CRC64;
Query Match 100.0%; Score 2633; DB 1; Length 514;
Best Local Similarity 99.6%; Pred. No. 1,4e-170;
Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSPPLSGAPGAEYLRAVLRAPVYEAQVTPLOQMEKLSRLDNVILVKEDRQPVHS 60
DB 1 MADSPPLSGAPGAEYLRAVLRAPVYEAQVTPLOQMEKLSRLDNVILVKEDRQPVHS 60
QY 61 FKLRGAYAMAGITTEBQKAGVITASAGNHAQVAFSSARLGVKALIVMPATADIKVDA 120
DB 61 FKLRGAYAMAGITTEBQKAGVITASAGNHAQVAFSSARLGVKALIVMPATADIKVDA 120
QY 121 VRFGGVEVLLHANPPEAKAKAIELSQOQGFVWPEFDPMTYAGOGTALATELQODAH 180
DB 121 VRFGGVEVLLHANPPEAKAKAIELSQOQGFVWPEFDPMTYAGOGTALATELQODAH 180

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QY 181 DRVFPVGGGGLAGVAVALIKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
DB 181 DRVFPVGGGGLAGVAVALIKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
QY 241 GVAVKRIDETFRLLCOEYLDDITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
DB 241 GVAVKRIDETFRLLCOEYLDDITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
QY 301 ALHNHGRRLAHIIISGANVNFHGLRYVSRCELSGOREALLAVTIPKSGFLKFCOLLG 360
DB 301 ALHNHGRRLAHIIISGANVNFHGLRYVSRCELSGOREALLAVTIPKSGFLKFCOLLG 360
QY 361 GRSVTEFNRYRPAADAKNACIFVGRVLSRGLSEKKEILLQMLNDGYSVDLSDDENAKLHYR 420
DB 361 GRSVTEFNRYRPAADAKNACIFVGRVLSRGLSEKKEILLQMLNDGYSVDLSDDENAKLHYR 420
QY 421 YWVGSRPSHPLOERLYSEFPESPGAKLRLNTLTGTWNISLFFHRSHTDYGRLAAFE 480
DB 421 YWVGSRPSHPLOERLYSEFPESPGAKLRLNTLTGTWNISLFFHRSHTDYGRLAAFE 480
QY 481 XGDHPDPETRLNELGYDCHDPTNNPARPFLAG 514
DB 481 XGDHPDPETRLNELGYDCHDPTNNPARPFLAG 514

RESULT 2
ID THDI_SALTY STANDARD; PRT; 514 AA.
AC P20506; Q9L6S8;
DT 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
DE deaminase).
GN ILVA OR STM3905 OR STM01.87.
OS Salmoneilla typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmoneilla.
OX NCBI_Taxid=602;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=88255870; PubMed=3290055;
RA Tallon B.E., Little R., Lawther R.P.;
RT "Analysis of the functional domains of biosynthetic threonine
RT deaminase by comparison of the amino acid sequences of three
RT wild-type alleles to the amino acid sequence of biodegradative
RT threonine deaminase."
RT Gene 63:245-252(1988).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RX Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RX Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E.,
RX Ryan E., Sun H., Florea L., Miller W., Stonking T., Nhan M.,
RX Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmoneilla enterica serovar Typhimurium
RT LT2."
RT Nature 413:852-856(2001).
RN [3]
RP SEQUENCE OF 1-10 FROM N.A.
RP STRAIN=LT2;
RX MEDLINE=89326124; PubMed=2473940;
RX Lopes J.M., Lawther R.P.;
RT "Physical identification of an internal promoter, ilvP, in the
RT distal portion of the ilvGMDA operon."
RT Gene 76:255-269(1989).
CC -!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydratation
CC of threonine, followed by rehydration and liberation of ammonia.
CC -!- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -!- COFACTOR: Pyridoxal phosphate.

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CC -!- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHEREAS
CC VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
CC -!- PATHWAY: Isoleucine biosynthesis; first step.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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CC -----
DR EMBL; M26570; AAA27150.1; -
DR EMBL; AF233324; AA933479.1; -
DR EMBL; AE008862; AAL22755.1; -
DR EMBL; M25498; AAA27151.1; -
DR PIR; J02078; DMBRTT.
DR HSSP; P04968; 1TDJ.
DR StyGene; SG10129; ilvA.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydratase.
DR InterPro; IPR005787; Thr_dehydratase.
DR InterPro; IPR001721; ThrDh_C.
DR Pfam; PF00291; PALP.1.
DR Pfam; PF00585; Thr_dehydrat_C_2.
DR TIGRFAMs; TIGR01124; ilvA_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
DR Isoleucine biosynthesis; lyase; Pyridoxal phosphate;
DR Allosteric enzyme; Complete proteome.
DR BINDING 62 62 PYRIDOXAL PHOSPHATE.
FT CONFLICT 71 71 A -> T (IN REF. 1).
FT CONFLICT 124 124 F -> L (IN REF. 1).
FT CONFLICT 339 339 A -> G (IN REF. 1).
FT CONFLICT 342 342 A -> T (IN REF. 1).
FT CONFLICT 351 353 SFL -> NFP (IN REF. 1).
SQ SEQUENCE 514 AA; 56253 MW; 136BC535F1F00358 CRC64;

Query Match 95.9%; Score 2525; DB 1; Length 514;
Best Local Similarity 95.1%; Pred. No. 2.7e-163;
Matches 489; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADQPLSGAGEGEYRAVLRAPVTEAQTPLQXKEKSSRLDNLVLYREORPVS 60
DB 1 MAEQPLSVAGEGAYLAVALRAPVTEAQTPLQXKEKSSRLDNLVLYREDBQVHS 60
QY 61 FKLGAAYMAGLTBEOKAHGVTITASAGNHQGVAFSSARLGVALIYPTATADIKYDA 120
DB 61 FKLGAAYMAGLTBEOKAHGVTITASAGNHQGVAFSSARLGVALIYPTATADIKYDA 120
QY 121 VRGEGEVLHGANFDEAKKVAIEISQOQGTWPPDPHVPVINGQTLAELLQODAH 180
DB 121 VRGEGEVLHGANFDEAKKVAIEIAQOQGTWPPDPHVPVINGQTLAELLQODSH 180
QY 181 DRVFPVGGGGLAGVAVALIKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
DB 181 DRVFPVGGGGLAGVAVALIKQMLPQIVIAVEADSDACLKAAADAGHPVDLPRVGLFAE 240
QY 241 GVAVKRIDETFRLLCOEYLDDITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
DB 241 GVAVKRIDETFRLLCOEYLDDITVDSDAICAMKDLFEDVRAVAEPGALALAGMKYI 300
QY 301 ALHNHGRRLAHIIISGANVNFHGLRYVSRCELSGOREALLAVTIPKSGFLKFCOLLG 360
DB 301 ALHNHGRRLAHIIISGANVNFHGLRYVSRCELSGOREALLAVTIPKSGFLKFCOLLG 360
QY 361 GRSVTEFNRYRPAADAKNACIFVGRVLSRGLSEKKEILLQMLNDGYSVDLSDDENAKLHYR 420
DB 361 GRSVTEFNRYRPAADAKNACIFVGRVLSRGLSEKKEILLQMLNDGYSVDLSDDENAKLHYR 420
QY 421 YWVGSRPSHPLOERLYSEFPESPGAKLRLNTLTGTWNISLFFHRSHTDYGRLAAFE 480
DB 421 YWVGSRPSHPLOERLYSEFPESPGAKLRLNTLTGTWNISLFFHRSHTDYGRLAAFE 480

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Db      421 YWVGRPSKPLQRLYSFEFEPSPGALLKFLHTLGTWNISLPHYRSHGTDYGRVLAAB 480
QY      481 XGDHEPDPETRLNELGYDCHDETNNPAFRPFLAG 514
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Db      481 LGDHEPDPETRLNELGYDCHDESSNPAFRPFLAG 514

RESULT 3
THD1_PASMU
ID      THD1_PASMU      STANDARD;      PRT;      513 AA.
AC      99CKJ2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
GN      deaminase).
GN      ILVA OR PM1624.
OC      Pasteurella multocida.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC      Pasteurellaceae; Pasteurella.
QX      NCBI_TaxId=747;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Pm70;
RX      MEDLINE=21145866; PubMed=11248100;
RA      May B.J., Zhang O., Li L.L., Paustian M.L., Whitam T.S., Kapur V.;
RT      "Complete genomic sequence of Pasteurella multocida Pm70."
RL      Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC      -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC      threonine in a two-step reaction. The first step is a dehydration
CC      of threonine, followed by rehydration and liberation of ammonia.
CC      -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC      -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -1- PATHWAY: Isoleucine biosynthesis; first step.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: AE006199; AK03708.1; -.
CC      DR      HSSP: P04968; ITD.
CC      DR      InterPro: IPR001926; B6_enzyme_beta.
CC      DR      InterPro: IPR000634; S/T_dehydratase.
CC      DR      InterPro: IPR005787; Thrdh_dehydratase.
CC      DR      InterPro: IPR001721; Thrdh_C.
CC      DR      Pfam: PF00281; PALP; 1.
CC      DR      Pfam: PF00585; Thrdh_dehydratase; 2.
CC      DR      TIGRPFAM: TIGR01124; Ilva_2Cterm; 1.
CC      DR      PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
CC      KW      Isoleucine biosynthesis; lyase; Pyridoxal phosphate;
CC      KW      complete proteome.
CC      FT      BINDING 61
CC      FT      SEQUENCE 513 AA; 56288 MW; 3E427ADC54E5FC7C CRC64;

Query Match      70.5%; Score 1857.5; DB 1; Length 513;
Best Local Similarity 69.4%; Pred. No. 33e-118;
Matches 352; Conservative 73; Mismatches 79; Indels 3; Gaps 3;

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Db      127 VLLHGANFDEAKAKAIELEASKMTFIPFPDHPAIVAGGSIAMELLQNSOIDRIFVAV 186
QY      188 GGGGLAAGVAVLIKQMLPOIKYIAVEADPSACLXALADGKVVDLPRVGLFEGVAVKRI 247
      :|||||:|||||:|||||:|||||:|||||:
Db      187 GGGGLAAGVAVLIKQMLPEIKYIAGESKOSACLYRALXKPKDIDRVGLFADGVAVKRI 246
QY      248 GDETFRLCOEYUDDITVDSDAICAMKDLFEDVAVAVAPSGALALAGKKYITALHNING 307
      :|||||:|||||:|||||:|||||:|||||:
Db      247 GDETFRLCOEYUDDITVDSDAICAMKDLFEDVAVAVAPSGALALAGKKYITALHNING 306
QY      308 ERLAHLISGANVNFHGLRVYSRCELGEORALLAVTTPEEKSGFLKFCOLLGKSVTER 367
      :|||||:|||||:|||||:|||||:|||||:
Db      307 ERLVAVLSGANVNFHGLRVYSRCELGEORALLAVTTPEEKSGFLKFCOLLGKSVTER 366
QY      368 NYRPADAKACITFVGVRSLRGLSEERKEILQMDGYSVVDLSDDEMAKLHYRVWVGR 427
      :|||||:|||||:|||||:|||||:|||||:
Db      367 KYRVADDKACITFVGVRSLRGLSEERKEILQMDGYSVVDLSDDEMAKLHYRVWVGR 425
QY      428 SHPLQRLYSFEFEPSPGAXLRFNLTLG-TYWNISLPHYRSHGTDYGRVLAABEXGDHBP 486
      :|||||:|||||:|||||:|||||:|||||:
Db      426 NSPLKERLYSFEFEPSPGAXLRFNLTLG-TYWNISLPHYRSHGTDYGRVLAABEXGDHBP 485
QY      487 D-PETRLNELGYDCHDETNNPAFRPFL 512
      :|||||:|||||:|||||:|||||:
Db      486 DAFNQHLEKLGYYQDVTESSPAYRYFL 512

RESULT 4
THD1_HAEIN
ID      THD1_HAEIN      STANDARD;      PRT;      513 AA.
AC      P46453;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
GN      deaminase).
GN      ILVA OR HI0738.1.
OC      Haemophilus influenzae.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC      Pasteurellaceae; Haemophilus.
QX      NCBI_TaxId=727;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Rd / KM20 / ATCC 51907;
RX      MEDLINE=95350630; PubMed=7542800;
RA      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA      Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA      McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA      Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA      Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA      Usterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
RA      Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
RA      Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA      Venter J.C.;
RT      "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT      Rd."
RL      Science 269:496-512(1995).
RN      [2]
RP      IDENTIFICATION.
RP      Koonin E.V., Rudd K.E.;
RL      Submitted (SEP-1995) to the SWISS-PROT data bank.
CC      -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC      threonine in a two-step reaction. The first step is a dehydration
CC      of threonine, followed by rehydration and liberation of ammonia.
CC      -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC      -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC      -1- PATHWAY: Isoleucine biosynthesis; first step.
CC      -1- SUBUNIT: Homodimer (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC      -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL; U32757; AAC22398.1; -
 DR HSSP; P04968; 1TDJ.
 DR TIGR; H10738.1; -
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/T dehydratase.
 DR InterPro; IPR005787; Thr dehydratase.
 DR Pfam; PFO0291; PALP; 1.
 DR Pfam; PFO0585; Thr dehydratase C; 2.
 DR TIGRFAMs; TIGR01124; 11vA_2Cterm; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 DR Isotransferase biosynthesis; Lyase; Pyridoxal phosphate;
 KW Complete proteome.
 KW BINDING 63
 KW SEQUENCE 513 AA; 56662 MW; DF42CA8B6FDE4CD7 CRC64;

Query Match 66.0%; Score 1738.5; DB 1; Length 513;
 Best Local Similarity 66.7%; Pred. No. 3.6e-110;
 Matches 337; Conservative 77; Mismatches 86; Indels 5; Gaps 4;

QY 11 PEGAEVRAVLR--APVYEAQVTPLOMELSSRLNVLIVKREDQPVHSFLKRGAY 68
 DB 10 PSQSDYINAIKGSRYVEAAQVTPLOMGLSSRLNHNVIKEDQPVHSFLKRGAY 69
 QY 69 MMAGLTEOKAGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGGEV 128
 DB 70 MISSLSAQKAGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGGEV 129
 QY 129 LHGANEDEAKAKAIEISQOQFTWPPFDHPVIAAGGTALIELLOQDAHLDEVPVVG 188
 DB 130 LHGANEDEAKAKAIEISQOQFTWPPFDHPVIAAGGTALIELLOQDAHLDEVPVVG 189
 QY 189 GGGGAAGVAVILKOLMPOIKVIAVEHDSACLKALADGHDVLDPRVGLFAGVAVRIG 248
 DB 190 GGGGAAGVAVILKOLMPOIKVIAVEHDSACLKALADGHDVLDPRVGLFAGVAVRIG 249
 QY 249 DETFRLCOEYLDITIVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGE 308
 DB 250 DETFRLCOEYLDITIVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGE 309
 QY 309 RLAIHLSGANVPHGLRVYSECEGEORALLAVTIPEEKSPFLKFCOLLGGRSVTEFN 368
 DB 310 RLAIHLSGANVPHGLRVYSECEGEORALLAVTIPEEKSPFLKFCOLLGGRSVTEFN 369
 QY 369 YRFADAKACIFVGVRLSRGIEERKEILQMLNDGYSVVDSDDEMAKLVHRYVWGRPS 428
 DB 370 YRFADAKACIFVGVRLSRGIEERKEILQMLNDGYSVVDSDDEMAKLVHRYVWGRPS 428
 QY 429 HPLERLYSFEPSPGAXLRFILNTLGTWNISLFHYRSHGTDYGRVLAFAEFGDHE--PD 487
 DB 429 ND-NERLYTFEPSPGAXLRFILNTLGTWNISLFHYRSHGTDYGRVLAFAEFGDHE--PD 487
 QY 488 FETRLNELGYDCHDETNNPAFRFL 512
 DB 488 FETRLNELGYDCHDETNNPAFRFL 512

RESULT 5
 THD1 BURCE STANDARD; PRT; 507 AA.
 AC P53607;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
 DN deaminase).
 ILVA.

OS Burkholderia cepacia (Pseudomonas cepacia).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Burkholderiaceae; Burkholderia.
 CC NCBI_TaxID=292;
 CC [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=17616;
 RA Bartell J.B., Lessie T.G.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
 CC threonine in a two-step reaction. The first step is a dehydration
 CC of threonine, followed by rehydration and liberation of ammonia.
 CC -1- CATALYTIC ACTIVITY: L-threonine + 2-oxobutanoate + NH(3).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Isotransferase biosynthesis; first step.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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DR EMBL; U40630; AAA83215.1; -
 DR HSSP; P04968; 1TDJ.
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/T dehydratase.
 DR InterPro; IPR005787; Thr dehydratase.
 DR InterPro; IPR001721; ThrDh_C.
 DR Pfam; PFO0291; PALP; 1.
 DR Pfam; PFO0585; Thr dehydratase C; 2.
 DR TIGRFAMs; TIGR01124; 11vA_2Cterm; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 DR Isotransferase biosynthesis; Lyase; Pyridoxal phosphate.
 KW BINDING 52
 KW SEQUENCE 507 AA; 55326 MW; E9A5D110B057664 CRC64;

Query Match 52.5%; Score 1383; DB 1; Length 507;
 Best Local Similarity 54.1%; Pred. No. 3.6e-86;
 Matches 273; Conservative 91; Mismatches 133; Indels 8; Gaps 5;

QY 15 EYLRAVRAVYEAQVTPLOMELSSRLNVLIVKREDQPVHSFLKRGAYMMAGLT 74
 DB 5 DYLRKILLAVYDVAFETELSPARNISARLRNVPYLLKREDQPVHSFLKRGAYMMAGLT 74
 QY 75 EEOKAHGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGG--EYLLH 131
 DB 65 ADALARGVITASAGNHAQVAFSSARLGVKALIVPTADIKVDVAGFGG--EYLLH 131
 QY 132 GANDEAKAKAIEISQOQFTWPPFDHPVIAAGGTALIELLOQ-DAHLDRVFPVGG 190
 DB 133 GANDEAKAKAIEISQOQFTWPPFDHPVIAAGGTALIELLOQ-DAHLDRVFPVGG 190
 QY 190 GGGGAAGVAVILKOLMPOIKVIAVEHDSACLKALADGHDVLDPRVGLFAGVAVRIG 248
 DB 191 GGGGAAGVAVILKOLMPOIKVIAVEHDSACLKALADGHDVLDPRVGLFAGVAVRIG 249
 QY 249 DETFRLCOEYLDITIVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGE 308
 DB 250 DETFRLCOEYLDITIVDSDAICAMKDLFEDVRAVAEPPSAGALAGMKYIALHNIRGE 309
 QY 309 RLAIHLSGANVPHGLRVYSECEGEORALLAVTIPEEKSPFLKFCOLLGGRSVTEFN 368
 DB 310 RLAIHLSGANVPHGLRVYSECEGEORALLAVTIPEEKSPFLKFCOLLGGRSVTEFN 369
 QY 369 YRFADAKACIFVGVRLSRGIEERKEILQMLNDGYSVVDSDDEMAKLVHRYVWGRPS 428
 DB 370 YRFADAKACIFVGVRLSRGIEERKEILQMLNDGYSVVDSDDEMAKLVHRYVWGRPS 428
 QY 429 HPLERLYSFEPSPGAXLRFILNTLGTWNISLFHYRSHGTDYGRVLAFAEFGDHE--PD 487
 DB 429 ND-NERLYTFEPSPGAXLRFILNTLGTWNISLFHYRSHGTDYGRVLAFAEFGDHE--PD 487
 QY 488 FETRLNELGYDCHDETNNPAFRFL 512
 DB 488 FETRLNELGYDCHDETNNPAFRFL 512

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DB 424 LDERLFRFFPPRPGALMKFLSSMAPDWNLSLFHRNQGADVSILVGLQVQADH-AEF 482
QY 489 ETRINELGYDCHDETNNPAFRFLA 513
DB 483 ERFALAGPYVEESANPAYRLFLS 507

RESULT 6
TIDH YEAST STANDARD; PRT; 576 AA.
AC P00927;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Threonine dehydratase, mitochondrial precursor (EC 4.3.1.19)
DE (Threonine deaminase).
ILV1 OR YER086W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
GN [1]
RP SEQUENCE FROM N.A.
RA Kjelland-Brandt M.C., Holmberg S., Petersen J.G.L.,
RA Nilsson-Tillgren T.;
RT "Nucleotide sequence of the gene for threonine deaminase (ILV1) of
RT Saccharomyces cerevisiae."
RT Carlberg Res. Commun. 49:567-575 (1984).
[2]
SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Huntke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Moseedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Borstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V."
RT Nature 387:78-81 (1997).
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHILE
CC VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
CC -1- PATHWAY: Isoleucine biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC
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CC
DR EMBL; M36383; AAA34705.1; -
DR EMBL; X01466; CAA25696.1; -
DR EMBL; U18839; AAB64641.1; -
DR PIR; S50589; DMBYT.
DR HSSP; P04968; ITDU.
DR SGD; S0000888; ILV1.
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR000634; S/P dehydratase.
DR InterPro; IPR005787; Thr dehydratase.
DR InterPro; IPR001721; ThDh_C.
DR Pfam; PF00291; PAUP; 1.
DR Pfam; PF00585; Thr dehydratase C; 2.
DR TIGRFAMs; TIGR01124; IlvA_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.

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KW Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;
KW Transaminase; Allosteric enzyme.
FT TRANSIT 1 576 MITOCHONDRION (POTENTIAL).
FT CHAIN ? 576 THREONINE DEHYDRATASE.
FT BINDING 109 109 PYRIDOXAL PHOSPHATE.
FT CONFLICT 259 259 I -> T (IN REF. 1).
SQ SEQUENCE 576 AA; 63831 MW; 0801BCBD7EEDC1F CRC64;

Query Match 46.1%; Score 1212.5; DB 1; Length 576;
Best Local Similarity 47.7%; Pred. No. 1.4e-74;
Matches 247; Conservative 99; Mismatches 147; Indels 25; Gaps 7;

QY 15 EYLRALVAPYEAQVTPLOKMEKSLRDNLVVKEDRQPHSEFLRGAYAMAGLT 74
DB 62 DYRLVRLSVYDVINESSPISQVGLSSRLNTNVLKEDLLPVSPFLRAGYNNIAKLD 121
QY 75 EEOKAGVITTSAGNAGVAFSSARLGVKLLIWPFTALIKYDANVGFGEVILLHGAN 134
DB 122 DSORQGVIAQSAGNAGVAFPAKHKLIPATIVPVCPSIKYQVSRILSQVVLGND 181
QY 135 FDEAKAKIELSOQGFPTWPPFDHPMVIAGQGLALELLOQDAHLDR---VFVPGGGG 191
DB 182 FDEAKAECAKLAERGLTNPFDHPPIYIAGQGLYAMEILRQVRANKIGAVFVPGGGG 241
QY 192 LAAGVAVLIKQLPQIKYIAVEABDSACKALADGHPVDLPRVGLFAEGVAVKRIQDET 251
DB 242 LIAGVAVLIKQVAPRIKILIGVETVDAATLHNSLQNRQTPLPVVGTFADGTSVEMIGET 301
QY 252 FRLCEYLDITITVDSDAICAMKDLFEDVAVVAPSPGALALAGKKYTA-LHNIRGRL 310
DB 302 FRVAQVVDDEVVLTVDICAAVVDIFEDTSSIVPSGALSVAGKKYISTVH---DEI 357
QY 311 AH-----ILSGAVNFGHRYVSERCLEGEORFALLAVTIPEKSGSLKFCOLLGSR 363
DB 358 DHTKATVPIILSGAMNDRLRFSERAVLGEKGVFMLVTLPRVGAFFKMGQKIHPRS 417
QY 364 VTEFNRYR-----ADAKNACIFVGVRLSGLEERKEILLQMLNDGYSVVDLSDDEMA 415
DB 418 VTEFSRYRNEHRESSVPRAYIYTSFVSVDREKEIKQVQQLNALFEAVDISDNEIRA 477
QY 416 KLVHRYMVGSRPSHLORLYSFEPSPGAXLRPLNTLGTWNLSLGHYSHGDXRY 475
DB 478 KSHGVYLVGASQKVP-NERRIISFEPPERGALTRFLGGLSGSWMLLPHRYNHGADIGKV 536
QY 476 LAAPFGDHP-DPETRINELGYDCHDETNNPAFRFL 512
DB 537 LAGISVPRENLTFOKFLIEDLGYTHDETNTVYQKL 574

RESULT 7
TIDH ARXAD STANDARD; PRT; 550 AA.
AC O42615;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DB Threonine dehydratase, mitochondrial precursor (EC 4.3.1.19)
DE (Threonine deaminase).
ILV1.
OS Arxula adeninivorans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
NCBI_TaxID=37620;
GN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS3;
RX MEDLINE=98398049; PubMed=9730281;
RA Wartmann T., Roessel H., Kunze I., Bode R., Kunze G.;
RT "Ilv1 gene from the yeast Arxula adeninivorans LS3 -- a new selective
RT transformation marker."
RT Yeast 14:1017-1025 (1998).
CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
CC -1- COFACTOR: Pyridoxal phosphate.

```

CC -1- PATHWAY: Isoleucine biosynthesis; first step.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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 CC
 DR EMBL: AJ222772; CAA10977.1; -.
 DR HSSP: P04968; ITDJ.
 DR InterPro: IPR001926; B6 enzyme beta.
 DR InterPro: IPR000634; S/T_dehydratase.
 DR InterPro: IPR005787; Thr_dehydratase.
 DR InterPro: IPR001721; ThrDh_C.
 DR Pfam: PF00291; PALP; 1.
 DR Trifam: PF00585; Thr dehydrat C; 2.
 DR Trifam: TIGR01124; jlvA-2Cterm; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
 DR KEGG: K01165; Lyase; Mitochondrion; Pyridoxal phosphate;
 KM Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;
 KM Transic peptide.
 FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
 FT CHAIN ? 550 THREONINE DEHYDRATASE.
 FT BINDING 86 86 PYRIDOXAL PHOSPHATE.
 FT SEQUENCE 550 AA; 60416 MW; D08CE5B55CC8A6F CRC64;
 SQ
 Query March 43.1%; Score 1136; DB 1; Length 550;
 Best Local Similarity 45.2%; Pred. No. 1.9e-69;
 Matches 236; Conservative 98; Mismatches 164; Indels 24; Gaps 9;
 QY 11 PEGA-EYLRAVLRAVYEAQVTPVLPQKMKSLSLNDVILVKREDROPVHSFKLGAAYAM 69
 DB 34 PDGTPDYLKILTSKVDVNCNETPVPVPAVNLSSKLGANIFLKRBDLPVSEFFKLKRGAYNM 93
 QY 70 MAGLTERQXKAGVTTASAGNHAQVAFSSARLGYKALIVMTATADIKNDAVRFGGEVL 129
 DB 94 MAHLPESTRKMGVAGSAGNHAQVAAVSAKGLNPATVWVPAKRYKVDRLGAKV 153
 QY 130 LHGANPEAKAKAIELEQQOQFTWVPFDPHPIVAGGTTALLETLOQ-DAH-IDRVFVPV 187
 DB 154 LHGNDPFAAKAECHRLSEKGLTNIPLFDNPYVLAGGTTIVELRLQIDVESLAIIVCI 213
 QY 188 GGGGLAAGVAVLTKQMPQIKVIAVEADSACLKAALDAGHPVDLPRVGLPAEGVAVKRI 247
 DB 214 GGGGLIAGVGAYIKRIAPQVKIIGETVDANAMQSLQKGRITLSEVGLFADGAAYKIL 273
 QY 248 GDEFFRLCOEYLDIITVDSALTCAMKDLFEDVRAVAEPGALALAGMKKTYLHNRG 307
 DB 274 GEEFFRLCOQVVDIVSTDEIAAKIDVTEFRSLVEPGALSVAGLVYVESH- 329
 QY 308 ERLAH-----LISGANVNFHGRVYSERCLEGEDEALLAVTIPERKSGFLFCQLG 360
 DB 330 PEITHSASGYTALISGANMDRLRFVSEKAKLEGESEVFVAITPEKPSFGGLIDLVA 389
 QY 361 GRASVTEFNYPADAK-----NACIFGVRLSRGLSEKELLQMLNDGQSVVDLSDDEM 414
 DB 390 PRAVTEFSYRSNGELEKSGDKAHVYISFVDNAKAEVRLIDDFKAGGFAIDISHNEF 449
 QY 415 AKLHVRTWGRBPHPL-QERLYSEFPPEPSGALRPLNTLGTWNISLFFYRSHGTDYG 473
 DB 450 PKSHPRYLVA-NQPTVNERVFRPEPERGALVKLHAGKSKWNTTLTFYRNQGSIDIA 507
 QY 474 RVLAPEKXGHEPD-FETRLNELGVDCHDETNNPAFRPFLAG 514
 DB 508 KYVLAGISVPSHSHSQFQGLDNLLEYPAAEETDNNVYKLFSG 549

ID THD1_ARATH STANDARD; PRT; 592 AA.
 AC Q9ZS6; Q9SPF1.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Threonine dehydratase biosynthetic, chloroplast precursor
 DE (EC 4.3.1.19) (threonine deaminase) (TD).
 GN OMRI OR AT3G10050 OR T22K18.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Columbia;
 RA Mourad G., Emerick R., Marion A., Smith A.;
 RT "Cloning and sequencing of a cDNA encoding threonine dehydratase/
 RT deaminase of Arabidopsis thaliana.";
 RL (in) Plant Gene Register PGR98-199.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mourad G.S., Smith A.M.;
 RT "Molecular characterization of the genomic clone, including the
 RT promoter sequences, of threonine dehydratase/deaminase from
 RT Arabidopsis thaliana.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, GM11b;
 RX MEDLINE=2014028; PubMed=10677454;
 RA Mourad G., Emerick R., Smith A.;
 RT "Molecular cloning and sequencing of a cDNA encoding an isoleucine
 RT feedback insensitive threonine dehydratase/deaminase of Arabidopsis
 RT thaliana line GM11b.";
 RL (in) Plant Gene Register PGR00-020.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Fatmoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
 RA Fatmann M., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delaney M., Boutry M., Grivell L.A., Mache R., Putdomenech P.,
 RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Catolico L., Weissenbach J., Saurin W., Querrier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs W., Benes V.,
 RA Wirtelmann E., Dizonak H., Erile H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehart T.-H., Nordsiek G.,
 RA Reichelt J., Scharte M., Schoen O., Bargues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Oltmawald B., Duchemin D.,
 RA Cooke R., Landie M., Berger-Plano C., Punelle B., Masny D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottelet A., Casacuberta E.,
 RA Monfort A., Argitiro A., Flores M., Liqiori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudi S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo W., Walts A., Ulteback T., Fujii C.Y., Shea T.P.,
 RA Creasey T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasamoto S., Kimura T., Ideasawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:820-822(2000).
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
 CC of threonine in a two-step reaction. The first step is a dehydration
 CC of threonine, followed by rehydration and liberation of ammonia.
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).

RESULT 8
 THD1_ARATH

84 NKPFGSDDELFOYVLDILASFPVDVAIESPLEIAKLSDRIGVNFYIKREDKORVFSFK 143
 QY 63 LGAVAMMAGLTTEOKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVR 122
 DB 144 LRGAIVMMNSLRRELDKGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVR 203
 QY 123 GFGGVLLHGANFDEAKAKAIEISQOOGFTWVPFDHVMVIAOGTTLAELLQODAHDR 182
 DB 204 ALGGVVLVYKGFDEAQTALHLEISKDGKXVPPDDPGVIAKGQGTIGTEINRQDKDIA 263
 QY 183 VFPVPGGGGLAGVAVLTKOLMPQIKVAVEAEDSACLAALDAGHPVDLPVGVAFAGV 242
 DB 264 VFIPVGGGLAGVAVTFPKQIAPNKKIGVEPYGASMTLSHEHRVYKLSVNDVFAAGV 323
 QY 243 AVKRGDETFPLCOEYLDIITVSDAICAMKDLFEDVRAVAFSSARLGVKALIVMPTATADIKVDAVR 302
 DB 324 AVAVGETTFACQGLIDGMVAVANDGISAATKDYDERNILETSAGVAILGAAYCEP 383
 QY 303 HNIRGERLAHLISGANVNFHGLRVYSECELOREBALLAVTIPEKGSPLKFCOLLGGR 362
 DB 384 YKIKENIVAILASGANMFESKLHKVTELAGSGKEALLATFPMVQGSFKTFVGLVGS 443
 QY 363 SVTEFNYP-ADAKNACIFVGRVLSRGLERKEIILQMLNDGYSVVDLSDDEMAKLVRY 421
 DB 444 NFEELTYFTSERKALILYRVNDKE--SDLEKMIEDKSSNMVTLNLSHRELVDHLKH 502
 QY 422 MYGGRPSHPLQERLY-SFEFPESPGAXLRFPLNTLGTWNISLFHYSRSHGTVGRVLAPE 480
 DB 503 LVGG--SANISPEIGEFIVPEKATLKTFLDAPSPRNMTITLCRRNQGDIASLIMGFO 560
 QY 481 XGDHEPD-FETRELGYDCHDETNNPAFPFLA 513
 DB 561 VPQAEDEPFKQADKLYPYELDNYNEAFNLVVS 594

RESULT 10
 THD1_CICAR STANDARD; PRT; 590 AA.
 AC 039469;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Threonine dehydratase biosynthetic, chloroplast precursor
 DE (EC 4.3.1.19) (Threonine deaminase) (TD).
 OS Cicer arietinum (Chickpea) (Garbanzo).
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosida I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OC NCBI_TaxId=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. PUSA 261 / PCITD 2, TISSUE=Seed;
 RX MEDLINE=95232188; PubMed=7716234;
 RA John S.J., Srivastava V., Guha-Mukherjee S.;
 RT "Cloning and sequencing of chickpea cDNA coding for threonine
 deaminase";
 RT Plant Physiol. 107:1023-1024 (1995).
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE (By
 similarity).
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.
 CC -1- SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -1- TISSUE SPECIFICITY: FOUND AT HIGHER LEVELS IN FLOWERS THAN IN
 OTHER ORGANS.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: X78575; CAAS5313.1; -
 CC PIR: T09532; T09532.
 DR HSSP: P04968; 1TDJ.
 DR InterPro: IPR001926; B6 enzyme_beta.
 DR InterPro: IPR000634; S/T dehydratase.
 DR InterPro: IPR005787; Thr dehydratase.
 DR InterPro: IPR001721; ThrDh_C.
 DR Pfam: PF00291; PALP; 1.
 DR Pfam: PF00585; Thr dehydratase C; 2.
 DR TIGRfams: TIGR01124; liva_2Cterm; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; FALSE NEG.
 KW Isoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal phosphate;
 KW Allosteric enzyme; Transic peptide.
 FT TRANSIT 1 44 CHLOROPLAST (POTENTIAL).
 FT CHAIN 45 590 THREONINE DEHYDRATASE BIOSYNTHETIC.
 FT BINDING 139 139 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 590 AA; 65153 MW; 01D7736AC92BCDEA CRC64;

Query Match 35.6%; Score 937.5; DB 1; Length 590;
 Best Local Similarity 41.5%; Pred. No. 5,4e-56;
 Matches 216; Conservative 92; Mismatches 178; Indels 35; Gaps 12;

QY 2 ADSQPLSGAPGCAEYLRVAVRPAVYEAQVTPLOKMEKLSRLDNVILYKREDQPVHSF 61
 DB 85 ADSDEL-----PEYLRLDVASLPYDVVESFVELTERLSRLGVNFVKKEDRQVPSF 138
 QY 62 KLRGAYMMAGLTTEOKAHGVITASAGNHAQGV--ASSARLGVKALIVMPTATADIKVDAVR 119
 DB 139 KLRGAYMMAGLTTEOKAHGVITASAGNHAQGV--ASSARLGVKALIVMPTATADIKVDAVR 198
 QY 120 AVRGFGVLLHGANFDEAKAKAIEISQOOGFTWVPFDHVMVIAOGTTLAELLQODAH 179
 DB 199 GVRLLGADVLMGTFDEAKTHAVELCKDGLRTITPEEDPAVIAKGQGTIGSEINRQDKR 258
 QY 180 LDRVFPVPGGGGLAGVAVLTKOLMPQIKVAVEAEDSACLAALDAGHPVDLPVGVAF 239
 DB 259 IDAVFVPVGGGGLAGVAVTFPKQIAPNKKIGVEPYGASMTLSHEHRVYKLSVNDVFAAGV 318
 QY 240 EGVAVKRGDETFPLCOEYLDIITVSDAICAMKDLFEDVRAVAFSSARLGVKALIVMPTATADIKVDAVR 299
 DB 319 DGATVAVGEYTFARCDVDVAVANDGISAATKDYDERNILETSAGVAILGAAYCEP 376
 QY 300 IALNIRGERLAHLISGANVNFHGLRVYSECELOREBALLAVTIPEKGSPLKFCOLL 359
 DB 377 CEMRIKNDNNVGVISGANMNFRLKHVSELAVALGSGHEALLGYTMPQKCFMTAGLV 436
 QY 360 -GGRSVTEFNYPFADAKNACIFVGRVLS--RGLERKEIILQMLNDGYSVVDLSDDEMAK 416
 DB 437 HGSLSPFTITRYTRFHSRSLIVMLKLEPMRYIE--KMIDMKYSGVTVANISHNELAV 493
 QY 417 LHAVRVMGGRPSHPLQERLY-SFEFPESPGAXL-RPLNTLGTWNISLFHYSRSHGTVGR 474
 DB 494 IHGKHLVGG--SAKVSDEVFEFIIPEK--ADLKKEFLEVLSPHNNLTLYRYRNOGDILKAT 549
 QY 475 VLAAPKXGDHEPD-----ETRLNELGYDCHDETNNPAFPFLA 508
 DB 550 ILWVIA-----FLCEIVIRKNDIIDGYEIDQYNDAP 584

RESULT 11
 THD1_SOLTU STANDARD; PRT; 359 AA.
 AC P31212;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine deaminase)
 DE (TD) (Fragment).
 GN TD.
 OS Solanum tuberosum (potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
 OK NCBI_TaxId=4113;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Desiree; TISSUE=leaf;
 RX MEDLINE=93005746; PubMed=1392612;
 RA Hildmann T., Ebneth M., Pena-Cortes H., Sanchez-Serrano J.J.,
 RA Willnitzer L., Prat S.;
 RA "General roles of abscisic and jasmonic acids in gene activation as a
 result of mechanical wounding.";
 RL Plant Cell 4:1157-1170(1992).
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanate + NH(3).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE.
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- TISSUE SPECIFICITY: FLORAL BUDS OF UNTREATED PLANTS. AFTER ABA
 TREATMENT OR MECHANICAL WOUNDING IS MOSTLY ACCUMULATED IN LEAVES.
 CC TO A LESSER EXTENT IN STEMS, BUT NOT IN ROOTS.
 CC -1- INDUCTION: BY ABSICISIC ACID (ABA), JASMONIC ACID (JA) AND
 WOUNDING.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X67846; CAA48039.1; -.
 DR PIR; P00468; P00468.
 DR HSSP; P04968; 1TDJ.
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/T dehydratase.
 DR InterPro; IPR001721; ThrdD_C.
 DR Pfam; PF00291; PALP; 1.
 DR Pfam; PF00585; Thr dehydratase C; 2.
 DR PROSITE; PS00165; DEHYDRATASE SER THR, PARTIAL.
 KM Isoleucine biosynthesis; lyase; Chloroplast; Pyridoxal phosphate;
 KM Allosteric enzyme.
 FT NON_TER 1
 FT SEQUENCE 359 AA; 39088 MW; 94DC75974AF9E830 CRC64;
 SQ
 . Query Match 24.4%; Score 642; DB 1; Length 359;
 . Best Local Similarity 38.8%; Pred. No. 2,6e-36;
 Matches 140; Conservative 68; Mismatches 147; Indels 6; Gaps 5;
 QY 156 PEDHENVIAAGGTLLELLQDADHVRVYVGGGGLAAGVALITQLMPOIVIAVEAE 215
 DB 1 PFDAPVIAKGGGTIGTEINNQLKDIAHAFVPGVGGGGLISGVAIFQVAPHTKIGVEPY 60
 QY 216 DSGCLKAALDAGRPVLLPRVGLFABGVAVYKIDETFERLCOEVLDDIITVDSALCAANK 215
 DB 61 GAASMTLISYEGHRAVLENDVTFADGVAALVGEYTPACKQELIDENVLFRNGGISAALK 120
 QY 276 DLEEDRAVAAPSGALALAGMKRYIALHNIRGRILHIIISGAVNPHGLRYVSECELES 335
 DB 121 DVADEGRNILETSGAVAIAGAAYCEFYNNKNNIYAIASGAMDSKILHKTVELAELOS 180
 QY 336 QREBALLAVTPEEKSGFLKCOLLGGRSVTEFYRP-ADAKNAICIVGVRLSGLEERKE 394
 DB 181 DNEALLATFEMIEQGFSEFKTPAKIVGSMNITEVTYRFTSEKELVLYRVDDVDE-KSDLER 239
 QY 395 ILQMLNDGGSVDLDSDDEAKLHVRYMGGRPSHPLQELTY-SPEFPEPQKXLAFLNT 453
 DB 240 MIRKLNSNNKTFNFHSHNLVAEHIKLVGSGAS--ISDEIFSEFIPPEAGTLSTFLER 297
 QY 454 LGTYNNISLPHYRSHGTDYGRVLAFAEXGDHPD-PETRLNELGYCHDETNNPARPFL 512

DB 298 FSPRNNITLCRYRDGDINGNLVVGFOVPOSEMEDEFSQADGLGYPELDNSNEAFNIVV 357
 QY 513 A 513
 DB 358 A 358
 RESULT 12
 ID THD1_BACSU STANDARD; PRT; 422 AA.
 AC P37946;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Threonine dehydratase biosynthetic (Ec 4.3.1.19) (Threonine
 deaminase).
 GN ILVA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OK NCBI_TaxId=1423;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Armpriester J.M. Jr., Fink P.S.;
 RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / Maiburg;
 RX MEDLINE=96349105; PubMed=8760912;
 RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
 RA Serror P.;
 RT "Sequence analysis of the Bacillus subtilis chromosome region between
 the serA and kds loci cloned in a yeast artificial chromosome.";
 RL Microbiology 142:2005-2016(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunert F., Ogasawara N., Moszer I., Albertini A.M., Allion G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Brouillet R., Boursier L., Brans A., Braun M., Brignall S.C., Bron S.,
 RA Brouillette S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Comerçon I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi N.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Bianhard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelie D., Porwollik S., Prescott A.M.,
 RA Presecan E., Puje P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivaletta C., Rochna E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeder R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccotti B., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vanderbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambut R., Wedler E., Wedler H., Weizenegger T., Yata K.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis".
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
 threonine in a two-step reaction. The first step is a dehydration
 of threonine, followed by rehydration and liberation of ammonia.
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanate + NH(3).

CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M58606; AAA22549.1; -
 DR EMBL; L77246; AAA96639.1; -
 DR EMBL; Z99115; CAB14095.1; -
 DR PIR; A69644; A69644.
 DR HSSP; P04968; ITD1.
 DR Subtilist; BG10673; 11VA.
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/T dehydratase.
 DR InterPro; IPR001721; Thrdh_C.
 DR Pfam; PF00291; PALP; 1.
 DR Pfam; PF00585; Thr dehydrat_C; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 DR Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
 DR Complete proteome.
 FT BINDING 60 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT CONFLICT 15 H -> D (IN REF. 2).
 FT CONFLICT 139 V -> A (IN REF. 2).
 FT SEQUENCE 422 AA; 46701 MW; 3027A5ED87084140 CRC64;
 SQ
 Query Match 24.4%; Score 642; DB 1; Length 422;
 Best Local Similarity 38.3%; Pred. No. 3.2e-36;
 Matches 149; Conservative 74; Mismatches 156; Indels 10; Gaps 7;
 QY 32 TPLQMKELSSRLDNVILVKREDROPVHSFKRGAYMMAGLTFEOKAHGVITASAGNHA 91
 D 30 TPLQMKELSSRLDNVILVKREDROPVHSFKRGAYMMAGLTFEOKAHGVITASAGNHA 89
 QY 92 QGVAFSSARLGVKALIVMPTATADIKVDVAVRGFG--EVLHGANDPEAKAKAIELSQ 148
 D 90 QGVAFSSARLGVKALIVMPTATADIKVDVAVRGFG--EVLHGANDPEAKAKAIELSQ 149
 QY 149 QGFTWVPFPHMPTVIAQGGTLALELQO--DAHMDRVVPVGGGAGLAVNLQMLPQI 207
 D 150 ESRFTHFDDPDVWAGGTLAVELNDIDTEPHFLFASVGGGGLSGVGYLLKNSPDT 209
 QY 208 KVIIVAEADSACLKALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 267
 D 210 KVIIVAEADSACLKALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 269
 QY 268 DATCAAMKDLFEDVRAVAEBSGALALAGMKKTYALAHNIRGERLAHLISGANVNFHGRYV 327
 D 270 GKVTCTSTIELNECAVVAEPAALSVAAIDLY--KDQIKGNVVCVSGGNNDIGRMQEM 327
 QY 328 SERELGEGORALLAVITPEKSGFLKF--CQLG--GASVTEFNRFADAK--NACIFGVYR 384
 D 328 KERLIIEGLOHYFTIVNPPORAGALREFLDVGLPNDIDITREFYTKNNKNSGPAVGIE 387
 QY 385 LSRGLERKEILLQMLNDGYSVVDLSDE 413
 D 388 L-QMKADYGPILERMNKKPFHYVEVKNDE 415
 RESULT 13
 THD1_BACHD STANDARD; PRT; 415 AA.
 AC O9K6C3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
 deaminase).

GN 11VA OR BH1711.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=6665;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H, Nakasone K, Takaki Y, Maeno G, Sasaki R, Masui N,
 RA Fuji F, Hirama C, Nakamura Y, Ogasawara N, Kuhara S,
 RA Horikoshi K;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
 CC threonine in a two-step reaction. The first step is a dehydration
 CC of threonine, followed by rehydration and liberation of ammonia.
 CC -1- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Isoleucine biosynthesis; first step.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AP001512; BAB05430.1; -
 DR PIR; G83863; G83863.
 DR HSSP; P04968; ITD1.
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/T dehydratase.
 DR InterPro; IPR001721; Thrdh_C.
 DR Pfam; PF00291; PALP; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 DR Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
 DR Complete proteome.
 FT BINDING 53 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT SEQUENCE 415 AA; 46469 MW; BF49D28B65C7CF2A CRC64;
 SQ
 Query Match 23.1%; Score 608; DB 1; Length 415;
 Best Local Similarity 34.7%; Pred. No. 6.2e-34;
 Matches 135; Conservative 87; Mismatches 157; Indels 10; Gaps 7;
 QY 32 TPLQMKELSSRLDNVILVKREDROPVHSFKRGAYMMAGLTFEOKAHGVITASAGNHA 91
 D 23 TPLQMKELSSRLDNVILVKREDROPVHSFKRGAYMMAGLTFEOKAHGVITASAGNHA 82
 QY 92 QGVAFSSARLGVKALIVMPTATADIKVDVAVRGFG--EVLHGANDPEAKAKAIELSQ 148
 D 83 QGVAFSSARLGVKALIVMPTATADIKVDVAVRGFG--EVLHGANDPEAKAKAIELSQ 142
 QY 149 QGFTWVPFPHMPTVIAQGGTLALELQO--DAHMDRVVPVGGGAGLAVNLQMLPQI 207
 D 143 HKMTFPHFPOEKVIAQGGTLAVELNDIDITFCISIGGGGLSGVGYLLKNSPDT 202
 QY 208 KVIIVAEADSACLKALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 267
 D 203 KVIIVAEADSACLKALDAGHPVDLPVGLFAEGVAVKRIQDETFRLCOEYLDIDITVDS 262
 QY 268 DATCAAMKDLFEDVRAVAEBSGALALAGMKKTYALAHNIRGERLAHLISGANVNFHGRYV 327
 D 263 GKICITTLINLYNQDAIVAEPAGAMPIALDEF--KDEIKGKTVCVSGGNNDIGRMQEM 320
 QY 328 SERELGEGORALLAVITPEKSGFLKF--CQLG--GASVTEFNRFADAK--NACIFGVYR 384
 D 321 KERLIIEGLOHYFTIVNPPORAGALREFLDVGLPNDIDITREFYTKNNKNSGPAVGIE 380
 QY 385 LSRGLERKEILLQMLNDGYSVVDLSDE 413

Db 381 LKCD-EDYHRLMDRLNKGFEYREINKNE 408

RESULT 14

THD1_LACLA STANDARD; PRT; 416 AA.
 AC Q02145; O34132; O9CG81;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Threonine dehydratase biosynthetic (EC 4.3.1.19) (threonine deaminase).
 GN ILVA OR IL1227.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 NCBI_TaxID=1360;
 RX MEDLINE=93015710; PubMed=1400210;
 RA Godon J.-J., Chopin M.-C., Ehrlich S.D.;
 RT "Branched-chain amino acid biosynthesis genes in Lactococcus lactis subsp. lactis";
 RT J. Bacteriol. 174:6580-6589(1992).
 (2)
 REVISIONS.
 RA Delorme C., Goupil-Feuillierat N., Godon J.-J., Ehrlich S.D.,
 RA Renault P.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 (3)
 SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RC MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Mincker P., Manger S., Jallion O., Malarme K.,
 RA Weisenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403";
 RT Genome Res. 11:731-753(2001).
 CC - FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.
 CC - CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
 CC - COFACTOR: Pyridoxal phosphate.
 CC - PATHWAY: Isoleucine biosynthesis; first step.
 CC - SUBUNIT: Homotetramer (by similarity).
 CC - SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
 CC EMBL: U92974; AAB81922.1; -
 CC EMBL: AE006354; AAK05325.1; -
 DR HSR, C86778; C86778.
 DR HSRP, P04968; 11DU.
 DR InterPro: IPR001926; B6_enzyme_beta.
 DR InterPro: IPR000634; S/T_dehydrase.
 DR InterPro: IPR001721; ThrDh_C.
 DR Pfam: PF00291; PALP; 1.
 DR Pfam: PF00585; Thr_dehydrat_C; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
 KW Isoleucine biosynthesis; lyase; Pyridoxal phosphate;
 KW Complete proteome.
 FT BINDING 51 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT CONFLICT 345 A -> S (IN REF. 1).
 FT CONFLICT 393 D -> N (IN REF. 1).
 FT CONFLICT 406 H -> R (IN REF. 1).
 SQ SEQUENCE 416 AA; 45577 MW; AFDA61464D7E977 CRC64;

Query Match 22.8%; Score 600; DB 1; Length 416;
 Best Local Similarity 37.4%; Pred. No. 2,2e-33;
 Matches 137; Conservative 73; Mismatches 142; Indels 14; Gaps 7;

QY 32 TPLOKMEKLSRLDNVILVRKEDROPVHSFPLRGAYAMAGITBOKAHGVITASAGNHA 91
 DB 21 TPLODLPYLSNKYQANTYLKEENLQKRSFYLKRGAYISIKLSDEGRSKGVYCASAGNHA 80
 QY 92 QGVAFSSARLVKALVMPATYADIKYDAVAFGE--VLLAGANFDEAKAKAIELSQ 148
 DB 81 QGVAFPAANQVINSATIEFVPTTPNQKISQVAFEGSSHVITILIGTIFDESARAAKAFSD 140
 QY 149 QGFTWVPFPHPMVYAGGTTALEL---QQDAHLDPVPVPGGGGIAAGVAVILKDM 204
 DB 141 NDKPFIDPFDDENYVAGGTALVLEFPAQAKQGISLDKIFVQIGGGGIIAGITAVSKERY 200
 QY 205 PQIKVIAVEARDSACTKALADAGHPVDLPRVGLFAEGVAVKRIGETFRLCOEYLDIT 264
 DB 201 PQTETIGVGAAGATSMKAYNSGQPVTLSEHIDKFPADGIAVATVQOKTQQLINDKYKOLLA 260
 QY 265 VDSDAICAMKDLFEDVRAVAPSGALALAGKKYIALHNI RGERLAHILSGANVPHGL 324
 DB 261 VDEGLISQTLIELVSKLGI VAEPAQATSVALL--LIKDEIKKNIYICITISGANNDISRM 318
 QY 325 RYVSERCELGQREALLAVTTIPEEKSGFLK-QLGLG-GRSVTEFN--RPADAKACIF 380
 DB 319 QEIERRAVYRGLKHYFVINFQRPQALRTVSDILGNDDITREYIKRADKGGPCL- 377
 QY 381 VGVRLS 386
 DB 378 VGILLS 383

RESULT 15

THD1_MYCTU STANDARD; PRT; 429 AA.
 AC Q10766;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine deaminase).
 GN ILVA OR RV1559 OR MT1610 OR MYCY48.06C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulterson J.E., Taylor K., Whitehead S., Barrall B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence";
 RT Nature 393:537-544(1998).
 (2)
 SEQUENCE FROM N.A.
 RP STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydration
CC of threonine, followed by rehydration and liberation of ammonia.
CC - CATALYTIC ACTIVITY: L-threonine = 2-oxobutanate + NH(3).
CC - COFACTOR: Pyridoxal phosphate (By similarity).
CC - PATHWAY: Isoleucine biosynthesis; first step.
CC - SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC
CC EMBL; Z74020; CAA98332.1; -
CC EMBL; AE007027; AAK45877.1; -
CC PIR; D70763; D70763.
CC HSSP; P04968; ITDJ.
CC TIGR; MT1610; -
CC
CC Tuberculin; Rv1559; -
CC InterPro; IPR001926; B6_enzyme_beta.
CC InterPro; IPR000634; S/T_dehydrtse.
CC InterPro; IPR001721; ThrDh_C.
CC Pfam; PF00291; PALP; 1.
CC Pfam; PF00585; Thr_dehydrat_C; 1.
CC PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
CC Isoleucine biosynthesis; lyase; Pyridoxal phosphate;
CC Complete proteome.
CC BINDING 66 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC FT DOMAIN 145 149 POLY-ALA.
CC FT DOMAIN 196 199 POLY-GLY.
CC SEQUENCE 429 AA; 45041 MW; DDC761EC258AC521 CRC64;

Query Match 22.0%; Score 578.5; DB 1; Length 429;
Best Local Similarity 32.3%; Pred. No. 6.4e-32;
Matches 170; Conservative 71; Mismatches 166; Indels 119; Gaps 15;

QY 4 SQPLSGAP---EGAEYRAVLR-APVEAAQVTPLOMEKLSRLDNVILVKREDROPV 58
Db 6 SQSPSSSPLFSLSGADIDRAAKRIAPV---VTPTPLQPSDRLSAITGATVYLKREDLQTV 62
QY 59 HSFLRGAVYAMWAGITTEQKHGVITASGNHAGVAFSSARLGKALIVMPTATADIKV 118
Db 63 RSYLRLGAVNLVQLSDDELALAGVAVSSAGNHAGFAVACRLGVHGRVVPARTPKQKR 122
QY 119 DAVRGFGE--VLLHGANPDEAKAKAIELESOQGSFTWVPFDPHVMVIAQGTLALELL- 174
Db 123 DRIYHGEFIDLVGSGSTVLLAAAALEDEYERGTATVPPFDLRTIAGGTTAVEVLG 182
QY 175 QODAHLDREVPVVGSGGILAGVAVILKQIMPQIKVIAVEADSACLKALDAGHPVDLPR 234
Db 183 QLEDEPDILVVPVGGGCIAGITTYLAERTNTNTAVLGEPAGAAAMMAALAAAGEPVTLDH 242
QY 235 VGLFAEGVAVRIQDETFRLCQEVLD--DITVSDAICAMKDLFEDVRAVAPBSGALA 292
Db 243 VDQFVDGAAVRAAGTLLVYALAAAGDWSLTFTVDEGAVCTAMLDLYONEGIIABPAGALS 302
QY 293 LAGMKKYYIALNIRGERLAHILSGANVVFHGLRVYSERCLEGEOREALLAVTIPEKGSF 352
Db 303 VAGILE-----ADIEPGSTV----- 317
QY 353 LKFCQLIGRSVTEFNRRFADAKNACIFVGVRLSRGLEERKEILLQMLNDGYSVVDLSD 412
Db 318 --VCLISGGNN-----DVSRYGEVLERSLVHLGLKHYFLVD----- 351
QY 413 EMATLHVRYVMGGRSHPLQERLYSFERPPSPGAKLRL-NTLGTWNISLFIHY-RSHGT 470
Db 352 -----FPQEPGALRRPLDVLGPNDDITLFEVYKRNRR 384
QY 471 DYGRVLAFAEXGDEHPDETRINEL-GYDCHDET---NNPAFRFPL 512

Db 385 ETGEALVGEIIGS-AAOLDGILAMRATDIHVEALPEGSPAYRYLL 429

Search completed: December 18, 2003, 15:28:48
Job time : 18 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 15:27:16 ; Search time 21 seconds
(without alignments)
2353.843 Million cell updates/sec

Title: NP418220
Perfect score: 2633
Sequence: 1 MADSQLSGAPEGAEYLRAV.....LGYDCHDETNNPAPRFLAG 514

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: PIR.76:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2633	100.0	514	1 DMECTS	threonine ammonia-
2	2622	99.6	514	2 B91217	threonine ammonia-
3	2575.5	97.8	515	2 C86063	threonine ammonia-
4	2520	95.7	514	2 AB0924	threonine ammonia-
5	2497	94.8	514	1 DMEBTT	threonine ammonia-
6	2349	85.4	514	2 AG0474	threonine ammonia-
7	1849.5	70.2	510	2 B83374	threonine ammonia-
8	1415.5	53.8	515	2 B83479	threonine ammonia-
9	1410.5	53.6	508	2 B81875	threonine ammonia-
10	1400.5	53.2	508	2 AB1147	threonine ammonia-
11	1380.5	52.4	568	2 E75502	threonine ammonia-
12	1354	51.4	504	2 F83603	threonine ammonia-
13	1318.5	50.1	503	2 A12334	threonine ammonia-
14	1306	49.6	508	2 S77559	threonine ammonia-
15	1212.5	46.1	576	1 DMEBTT	threonine ammonia-
16	1123.5	42.7	600	2 T35116	threonine ammonia-
17	1087	41.3	592	2 T51712	threonine ammonia-
18	994.5	37.8	595	2 A18628	threonine ammonia-
19	937.5	35.6	590	2 T09532	probable threonine
20	646	24.5	422	2 A65644	threonine ammonia-
21	642	24.4	359	2 PQ0468	threonine ammonia-
22	632	23.2	441	2 S35141	probable threonine
23	608	23.1	415	2 G83863	threonine ammonia-
24	600	22.8	416	2 C86778	threonine ammonia-
25	594	22.6	422	2 C89998	threonine ammonia-
26	590.5	22.4	422	2 AG1323	threonine dehydrat
27	580.5	22.0	416	2 F97922	dihydroxy-acid deh
28	580.5	22.0	416	2 B95052	threonine dehydrat
29	578.5	22.0	429	2 D70763	threonine ammonia-

30	577.5	21.9	422	2 AH1694	threonine dehydrat
31	577	21.9	427	2 C87060	threonine deaminas
32	566	21.5	495	2 H84359	threonine dehydrat
33	558.5	21.2	403	2 D81355	threonine ammonia-
34	556	21.1	401	2 D72386	threonine ammonia-
35	551	20.9	419	2 A13368	threonine ammonia-
36	549	20.9	436	2 A47044	threonine ammonia-
37	533	20.2	329	2 AB0897	threonine ammonia-
38	529	20.1	329	1 DMECTD	threonine ammonia-
39	529	20.1	329	2 D85973	threonine ammonia-
40	529	20.1	329	2 E91128	threonine ammonia-
41	521	19.8	424	2 AB2725	threonine dehydrat
42	521	19.8	437	2 F97506	threonine dehydrat
43	516	19.6	405	2 D90166	hypothetical prote
44	512.5	19.5	400	2 AB7700	threonine dehydrat
45	512	19.4	320	2 E83310	L-serine ammonia-1

ALIGNMENTS

RESULT 1

DMECTS
threonine ammonia-lyase (EC 4.3.1.19), biosynthetic - Escherichia coli (strain K-12)
N:Alternate names: L-serine dehydratase; serine deaminase; threonine deaminase
C:Species: Escherichia coli
C>Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text change 21-Jun-2002
C:Accession: B27310; C26287; E26570; S48895; S30670; I41504; G65180
R:COX, J.L.; Cox, B.D.; Fidanza, V.; Calhoun, D.H.
Gene 56, 185-198, 1987
A:Title: The complete nucleotide sequence of the ilvGMDA cluster of Escherichia coli K-
A:Reference number: A91578; MUID:88056322; PMID:3315862
A:Accession: B27310
A:Molecule type: DNA
A:Residues: 1-514 <COX>
A:Cross-references: GB:M32253
A:Experimental source: Strain K12
R:Wek, R.C.; Hatfield, G.W.
J. Biol. Chem. 261, 2441-2450, 1986
A:Title: Nucleotide sequence and in vivo expression of the ilvY and ilvC genes in Escher-
A:Reference number: A92575; MUID:86111952; PMID:3303115
A:Accession: C26287
A:Molecule type: DNA
A:Residues: 439-514 <WEK>
A:Cross-references: GB:K03503
A:Experimental source: Strain K12
R:Lawther, R.P.; Wek, R.C.; Lopes, J.M.; Pereira, R.; Tailon, B.E.; Hatfield, G.W.
Nucleic Acids Res. 15, 2137-2155, 1987
A:Title: The complete nucleotide sequence of the ilvGMDA operon of Escherichia coli K-1
A:Reference number: A26570; MUID:87174741; PMID:3550695
A:Accession: E26570
A:Molecule type: DNA
A:Residues: 1-242, 'G', 244-514 <LAW1>
A:Cross-references: GB:M32253; NID:G146465; PIDN:AAA24024.1; PID:G146470
R:Lawther, R.P.
submitted to the EMBL Data Library, December 1987
A:Reference number: S48893
A:Accession: S48895
A:Molecule type: DNA
A:Residues: 1-514 <LAW2>
A:Cross-references: EMBL:X04890; NID:G288528; PIDN:CAA28577.1; PID:G288533
A:Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 t
Science 257, 771-778, 1992
R:Danielis, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
A:Reference number: S30670; MUID:92358234; PMID:1379743
A:Accession: S30670
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-121, 'X', 123-139, 'R', 141-514 <DAN>
A:Cross-references: EMBL:M87049; NID:G836656; PIDN:AAA67575.1; PID:G148179
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
R:Lopes, J.M.; Lawther, R.P.
Gene 76, 255-269, 1989

A/Title: Physical identification of an internal promoter, ilvAp, in the distal portion of
A/Reference number: I41304; MWID:89326124; PMID:2473940
A/Accession: I41304
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-10 <RSS>
A/Cross-references: GB:425497; NID:9341363; PIDN:AAA24015.1; PID:9538347
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MWID:97426617; PMID:9278503
A/Accession: G65180
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1514 <BLAT>
A/Cross-references: GB:AE000453; GB:U00096; NID:92367276; PIDN:AACT7492.1; PID:91790207;
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A:Gene: ilvA
A:Map position: 85 min
C/Function:
A/Description: catalyzes the deamination of threonine to yield alpha-ketobutyrate and am
A/Pathway: isoleucine-valine biosynthesis
A/Note: this is the first enzyme in the isoleucine biosynthetic pathway
C/Superfamily: threonine dehydratase
C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; isol
F/2/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 100.0%; Score 2633; DB 1; Length 514;
Best Local Similarity 99.6%; Pred. No. 1.2e-176;
Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MADSQPLSGAPGAEYLRVLRAPVYEAQVPLQKMEKLSRLDNVILVKREDROPVHS 60
DB 1 MADSQPLSGAPGAEYLRVLRAPVYEAQVPLQKMEKLSRLDNVILVKREDROPVHS 60
QY 61 FKLRGAYNMAAGLTHEOKAHGVTASAGNHAQVAFSSARLGVKALIVMTATADIKVA 120
DB 61 FKLRGAYNMAAGLTHEOKAHGVTASAGNHAQVAFSSARLGVKALIVMTATADIKVA 120
QY 121 VRFGEVLLHGANPDEAKAKAIELSQOQGFVWPFPDHPMTIAGCTLALBLQDADL 180
DB 121 VRFGEVLLHGANPDEAKAKAIELSQOQGFVWPFPDHPMTIAGCTLALBLQDADL 180
QY 181 DRFPVVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKALDAGHPVDLPRVGLFAE 240
DB 181 DRFPVVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKALDAGHPVDLPRVGLFAE 240
QY 241 GVAVRIGETFRLOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKKYI 300
DB 241 GVAVRIGETFRLOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKKYI 300
QY 301 ALHNIRGERLAHILSGANNFHLGRVYSERCLEGEORREALLAVTIPBEKGSFLKCOLLG 360
DB 301 ALHNIRGERLAHILSGANNFHLGRVYSERCLEGEORREALLAVTIPBEKGSFLKCOLLG 360
QY 361 GRSVTEFNRFADAKNACIFVGVRLSRGLEERKEILQMLNDGYSVVDLSDDMAKLHVR 420
DB 361 GRSVTEFNRFADAKNACIFVGVRLSRGLEERKEILQMLNDGYSVVDLSDDMAKLHVR 420
QY 421 YWVGGRPSHPLOERLYSFEPPSPGAXLRFLNTLGTWNISLFHYSHGTDGRVLAAP 480
DB 421 YWVGGRPSHPLOERLYSFEPPSPGAXLRFLNTLGTWNISLFHYSHGTDGRVLAAP 480
QY 481 XGDHBDPFTRLNELGYDCHDETNNPAPFRFLAG 514
DB 481 XGDHBDPFTRLNELGYDCHDETNNPAPFRFLAG 514

RESULT 2
B91217
threonine ammonia-lyase (EC 4.3.1.19) [similarity] - *Escherichia coli* (strain O157:H7, S

C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Aug-2002
C/Accession: B91217
R/Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
Gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genc
A/Reference number: A99629; MWID:21156231; PMID:11258796
A/Accession: B91217
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-514 <HAY>
A/Cross-references: GB:BA000007; PIDN:BA38129.1; PID:91364181; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RIMD 0509352
C/Genetics:
A:Gene: EC64706
C/Superfamily: threonine dehydratase
C/Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 99.6%; Score 2622; DB 2; Length 514;
Best Local Similarity 99.2%; Pred. No. 7.2e-176;
Matches 510; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 MADSQPLSGAPGAEYLRVLRAPVYEAQVPLQKMEKLSRLDNVILVKREDROPVHS 60
DB 1 MADSQPLSGAPGAEYLRVLRAPVYEAQVPLQKMEKLSRLDNVILVKREDROPVHS 60
QY 61 FKLRGAYNMAAGLTHEOKAHGVTASAGNHAQVAFSSARLGVKALIVMTATADIKVA 120
DB 61 FKLRGAYNMAAGLTHEOKAHGVTASAGNHAQVAFSSARLGVKALIVMTATADIKVA 120
QY 121 VRFGEVLLHGANPDEAKAKAIELSQOQGFVWPFPDHPMTIAGCTLALBLQDADL 180
DB 121 VRFGEVLLHGANPDEAKAKAIELSQOQGFVWPFPDHPMTIAGCTLALBLQDADL 180
QY 181 DRFPVVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKALDAGHPVDLPRVGLFAE 240
DB 181 DRFPVVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKALDAGHPVDLPRVGLFAE 240
QY 241 GVAVRIGETFRLOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKKYI 300
DB 241 GVAVRIGETFRLOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKKYI 300
QY 301 ALHNIRGERLAHILSGANNFHLGRVYSERCLEGEORREALLAVTIPBEKGSFLKCOLLG 360
DB 301 ALHNIRGERLAHILSGANNFHLGRVYSERCLEGEORREALLAVTIPBEKGSFLKCOLLG 360
QY 361 GRSVTEFNRFADAKNACIFVGVRLSRGLEERKEILQMLNDGYSVVDLSDDMAKLHVR 420
DB 361 GRSVTEFNRFADAKNACIFVGVRLSRGLEERKEILQMLNDGYSVVDLSDDMAKLHVR 420
QY 421 YWVGGRPSHPLOERLYSFEPPSPGAXLRFLNTLGTWNISLFHYSHGTDGRVLAAP 480
DB 421 YWVGGRPSHPLOERLYSFEPPSPGAXLRFLNTLGTWNISLFHYSHGTDGRVLAAP 480
QY 481 XGDHBDPFTRLNELGYDCHDETNNPAPFRFLAG 514
DB 481 XGDHBDPFTRLNELGYDCHDETNNPAPFRFLAG 514

RESULT 3
C86063
threonine ammonia-lyase (EC 4.3.1.19) [similarity] - *Escherichia coli* (strain O157:H7, S
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Aug-2002
C/Accession: C86063
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, B.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: AB5480; MWID:21074935; PMID:11206551
A/Accession: C86063
A/Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-515 <STO>
 A:Cross-references: GB:A0005174; NID:g12518630; PIDN:AA658967.1; GSPDB:GN00145; UMGF:Z55
 A:Experimental source: strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ilvA
 C:Superfamily: threonine dehydratase
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 97.8%; Score 2575.5; DB 2; Length 515;
 Best Local Similarity 98.1%; Pred. No. 1.3e-172;
 Matches 505; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

```

Oy 1 MADSPISGAPGAGAYLRAVLRAPVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHS 60
Db 1 MADSPISGAPGAGAYLRAVLRAPVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHS 60
Oy 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Db 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Oy 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Db 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Oy 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Db 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Oy 181 DRVFPVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLFAE 240
Db 181 DRVFPVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLFAE 240
Oy 241 GVAVKRIGDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Db 241 GVAVKRIGDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Oy 301 ALHNIRGERLAHIIISGANVNFHGLRYVSECELGEOREALLAVTIPEKSGFLKFCOLL 359
Db 301 ALHNIRGERLAHIIISGANVNFHGLRYVSECELGEOREALLAVTIPEKSGFLKFCOLL 359
Oy 360 GRSVTEFNYPADAKNAICIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVHR 419
Db 360 GRSVTEFNYPADAKNAICIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVHR 419
Oy 420 RYMVGGRPSHPLOEIRLYSEFPESPGAKLRFPLNTLGTWNISLFYRSHGTDYGVLAFAE 479
Db 420 RYMVGGRPSHPLOEIRLYSEFPESPGAKLRFPLNTLGTWNISLFYRSHGTDYGVLAFAE 479
Oy 480 EXGDHEPDPETRLNGLGYDCHDETNNPAFRPFLAG 514
Db 480 EXGDHEPDPETRLNGLGYDCHDETNNPAFRPFLAG 514

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RESULT 4

AB0924
 threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Salmonella enterica subsp. enterica
 C:Species: Salmonella enterica subsp. enterica serovar Typhimurium
 A:Note: this species has also been called Salmonella typhimurium
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AB0924
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
 A:Reference number: AB0924; MUID:21534947; PMID:11677608
 A:Accession: AB0924
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-514 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD09412.1; PID:g16504530; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3652
 C:Superfamily: threonine dehydratase
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 95.7%; Score 2520; DB 2; Length 514;
 Best Local Similarity 94.9%; Pred. No. 1e-168;
 Matches 488; Conservative 18; Mismatches 8; Indels 0; Gaps 0;

```

Oy 1 MADSPISGAPGAGAYLRAVLRAPVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHS 60
Db 1 MADSPISGAPGAGAYLRAVLRAPVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHS 60
Oy 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Db 61 FKLNGAYAMMAGLTREQKAGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVA 120
Oy 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Db 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Oy 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Db 121 VRGSGEVLHGAFNDEKAKAIELSQOQGFVTPPDHPVNIAGQTLAELAQDPAHL 180
Oy 181 DRVFPVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLFAE 240
Db 181 DRVFPVGGGGLAAGVAVLIKQMPQIKVIAVEADSACLKAALDAGHPVDLPVGLFAE 240
Oy 241 GVAVKRIGDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Db 241 GVAVKRIGDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEESGALALAGMKKYI 300
Oy 301 ALHNIRGERLAHIIISGANVNFHGLRYVSECELGEOREALLAVTIPEKSGFLKFCOLL 360
Db 301 ALHNIRGERLAHIIISGANVNFHGLRYVSECELGEOREALLAVTIPEKSGFLKFCOLL 360
Oy 361 GRSVTEFNYPADAKNAICIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVHR 420
Db 361 GRSVTEFNYPADAKNAICIFGVRLSRGLEERKEIILQMLNDGYSVVDLSDEMAKLVHR 420
Oy 421 YMVGRPSHPLOEIRLYSEFPESPGAKLRFPLNTLGTWNISLFYRSHGTDYGVLAFAE 480
Db 421 YMVGRPSHPLOEIRLYSEFPESPGAKLRFPLNTLGTWNISLFYRSHGTDYGVLAFAE 480
Oy 481 XGDHEPDPETRLNGLGYDCHDETNNPAFRPFLAG 514
Db 481 XGDHEPDPETRLNGLGYDCHDETNNPAFRPFLAG 514

```

RESULT 5

DWERT
 threonine ammonia-lyase (EC 4.3.1.19), biosynthetic - Salmonella typhimurium
 N:Alternate names: L-serine dehydratase; serine deaminase; threonine deaminase
 C:Species: Salmonella typhimurium
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jun-2002
 C:Accession: J0278
 R:Tallion, B.E.; Little, R.; Lawther, R.P.
 Gene 63, 245-252, 1988
 A:Title: Analysis of the functional domains of biosynthetic threonine deaminase by complementation
 A:Reference number: J0278; MUID:88255870; PMID:3230055
 A:Accession: J0278
 A:Molecule type: DNA
 A:Residues: 1-514 <TAI>
 A:Cross-references: GB:M26670; NID:g341512; PIDN:AAA27150.1; PID:g514966
 A:Note: the authors translated the codon CTG for residue 169 as Ile
 C:Genetics:
 A:Gene: ilvA
 A:Map position: 83 min
 C:Function: catalyzes the deamination of threonine to yield alpha-ketobutyrate and ammonia
 A:Description: catalyzes the deamination of threonine to yield alpha-ketobutyrate and ammonia
 A:Pathway: isoleucine-valine biosynthesis
 A:Note: this is the first enzyme in the isoleucine biosynthetic pathway
 C:Superfamily: threonine dehydratase
 C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; isol
 P:62/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 94.8%; Score 2497; DB 1; Length 514;
 Best Local Similarity 94.0%; Pred. No. 4.1e-167;
 Matches 483; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

253 RLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALNINIGERLAAH 312
248 RLCOQYIDGHVTVSSDEICAAVKDIFEDTRAIAPSPGALALAGKFAEQOQLKGQLT 307
313 ILSGANNVPHGLRYVSECEGEORREALLATIPEEKSPFKCOLLGGSVTEFNTREFA 372
308 VLSGANNVPHGLRYVSECEGEORREALLATIPEEKSPFKCOLLGGSVTEFNTREFA 367
373 DAKNACIFVGRVRLSGLEERKEILQMLNDGYSVVDLSDDEMAKTLHVRVYVWGGRPSHP 432
368 DDQLANIVGVRLVGGPELKSITHELRQSGYPIVQDSDDEMAKTLHVRVYVWGGRPSHP 427
433 ERLVSFEPPESPGAXLRLPLNTIGTYWNISLPHYRSHGTDYGRVLAPEXGDHEPD--FE 489
428 ERLVSFEPPESPGAXLRLPLNTIGTYWNISLPHYRSHGTDYGRVLAPEXGDHEPD--FE 485
490 TRINELGYDCHDETNNPAFFFLA 513
486 EHLVELGYRYKDETDNPAFFFLA 509

RESULT 8

B83479
threonine dehydratase, biosynthetic PA1326 [imported] - Pseudomonas aeruginosa (strain F
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Jun-2002
C:Accession: B83479
R:Stover, C.K.; Plam, X.O.; Eryin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83479
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <STD>
A:Cross-references: GB:AE004562; GB:AE004091; NID:99947263; PIDN:AG04715.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: llyA2; PA1326
A:Superfamily: threonine dehydratase

Query Match 53.8%; Score 1415.5; DB 2; Length 515;
Best Local Similarity 54.4%; Pred. No. 2.2e-91;
Matches 279; Conservative 95; Mismatches 132; Indels 7; Gaps 3;

1 MADSQPLSGAEGAEYLRARVYEAQVTPLOKMEKLSRLDNLVLRKEDROPVHS 60
6 LSAKPLL-----AGYASIIAAFPYDVAVETPLQVAPQLSQRNLKRELDLPVFS 60
61 FKLKGAAYAMAGLTBEQQAHVITASAGNAQVAFSSARLGVKALYMPATADIKYDA 120
61 FKIGAYTRVARLDEQCARGVITASAGNHAQGLAALQRLGVRAVYVMPPTPELKYG 120
121 VRGGEVTLHGANPDEAKATIELSQOQGFVWPDPHPVITAGGTLAELIQD--DAH 179
121 VLAAGGELLHGDAPDMLAHLQLAERGMTFVPDPDPAVIAAGGTVAWEILRHSGR 180
180 LDRVFPVGGGLAGAVALLKOLMPOIKVIAVEASACIKALLDGHPVDLPRVGLFA 239
181 LDAIFVPVGGSLIAGIAAYVGHLPDIRIVGPEPDSNCQALALAAGERVAVLQVGLFA 240
240 EGVAVKRGDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRY 299
241 DGVVAQIAGACNFECVKDHDVETVGSDEICAAIKDITDTRSTTEPAGALAAVAGIKY 300
300 IALNINIGERLAAHLSGANNVPHGLRYVSECEGEORREALLATIPEEKSPFKCOLL 359
301 VABERTEQTLVALDSGANNINFDRLRHAERAEIGEORREALIATVVAERPSFAFCAL 360
360 GGRSVTEFNYPADAKNACIFVGRVRLSGLEERKEILQMLNDGYSVVDLSDDEMAKTLH 419

Db 361 GRROITEFNRYHSDQAHFVGVQTHPLTDSRADLILAGEQGFVPLDLTDNEMAKLHI 420
Qy 420 RYVWGGRRPSPHLERLYSFEPPESPGAXLRLPLNTIGTYWNISLPHYRSHGTDYGRVLA 479
Db 421 RHWVGHGTEVRERKRLREFEPPERPGALRLPLNTIGTYWNISLPHYRSHGTDYGRVLA 480
Qy 480 EXGDHE-PDEPTRLNELYDCHDETNNPAFFFLA 511
Db 481 QVPEERGELEALQALIGYVWETINPAFFFLA 513

RESULT 9

B81875
threonine ammonia-lyase (EC 4.3.1.19) NMA1096 [similarity] - Neisseria meningitidis (stre
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jun-2002
C:Accession: B81875
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rasmussen,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81875; MUID:20222556; PMID:10761919
A:Accession: B81875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA84359.1; PID:g7379791
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: llyA; NMA1096
A:Superfamily: threonine dehydratase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos
P;56/Binding site: pyridoxal phosphate (lye) (covalent) #status predicted

Query Match 53.6%; Score 1410.5; DB 2; Length 508;
Best Local Similarity 55.6%; Pred. No. 4.8e-91;
Matches 280; Conservative 85; Mismatches 132; Indels 7; Gaps 4;

14 AEYLRARVYEAQVTPLOKMEKLSRLDNLVLRKEDROPVHSFKLRGAYAMAGL 73
8 SNYLIRLTASVYDVAVETPLQVAPQLSQRNLKRELDLPVFSFKLRGAYAMAGL 67
74 TEBOKAHGVITASAGNHAQVAFSSARLGVKALYMPATADIKYDAVVRGGEVTLHGA 133
68 PKALACGVTAASAGNHAQVAFSSARLGVKALYMPATADIKYDAVVRGGEVTLHGA 127
134 NPEAKKATIELSQOQGFVWPDPHPVITAGGTLAELIQD--RVFVPGGG 190
128 SYNDAYDYAMELAEQGLTYIAFPDPAVIAAGGTVAWEILRHSGR 185
191 GLAAGVAVLTKOLMPOIKVIAVEASACIKALLDGHPVDLPRVGLFAEGVAVKRGIDE 250
186 GLAAGVAVLTKOLMPOIKVIAVEASACIKALLDGHPVDLPRVGLFAEGVAVKRGIDE 245
251 TPRLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALNINIGERL 310
246 TPRLCOEYLDITVDSDAICAMKDLFEDVRAVAPSGALALAGKRYTALNINIGERL 305
311 AHILSGANNVPHGLRYVSECEGEORREALLATIPEEKSPFKCOLLGGSVTEFNTREFA 370
306 IAVTSAGNNVPHGLRYVSECEGEORREALLATIPEEKSPFKCOLLGGSVTEFNTREFA 365
371 PADAKNACIFVGRVRLSGLEERKEILQMLNDGYSVVDLSDDEMAKTLHVRVYVWGGRPSHP 430
366 YGDEKRAHIFVGLQ--AAGPDQDLAVISGRIDEALPVDLTDDEIAHIRYVWGGRRDKV 424
431 LOERLVSFEPPESPGAXLRLPLNTIGTYWNISLPHYRSHGTDYGRVLAPEXGDHE-PDE 489
425 ENERLVSFEPPESPGAXLRLPLNTIGTYWNISLPHYRSHGTDYGRVLAPEXGDHE-PDE 484
490 TRINELGYDCHDETNNPAFFFLA 513
485 GFLSLGYSYHEETQNAAYLFLA 508

RESULT 10

A81147

theonine ammonia-lyase (EC 4.3.1.19) NMB0878 [similarity] - *Neisseria meningitidis* (str C) Species: *Neisseria meningitidis*

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jun-2002

C/Accession: A81147

R/Retcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiatani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.;

A/Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A/Reference number: A81000; MUID:2015755; PMID:10710307

A/Accession: A81147

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-508 <RET>

A/Cross-references: GB:AE002440; GB:AE002098; NID:97226112; PIDN:AAF41289.1; PID:9722611

A/Experimental source: serogroup B, strain MC58

C/Genetics:

A/Genes: NMB0878

C/Suprafamily: theonine dehydratase

C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos

F;56/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 53.2%; Score 1400.5; DB 2; Length 508;

Best Local Similarity 55.0%; Pred. No. 2,4e-90;

Matches 277; Conservative 89; Mismatches 131; Indels 7; Gaps 4;

14 AEYLAVLRAPVYEAQVTPLOKMEKLSRLDNVILVKREDROPVHSFKRGVYAAWAGI 73

8 SDPLRLILTSVVDVAVETPPLPARSLSVLKNILKREDLPVHSFKRGVYAAWAGI 67

74 TEQKAGHGVITTAAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGFEVLLHGA 133

68 PKHALACGVIAASAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGFEVLLHGA 127

134 NDEAKAKATELSQOQGFVTPPDHVPVIAAGGTTALELLODAHLN--RVFVVGQ 190

128 SYNDADVAMELEKEGLTYIAEPDDPVDVIAAGGTTALELLODAHLN--RVFVVGQ 185

191 GLAAGVAVILKOLMPOIKVIAVEADSAICKALDGHPRVDFAGVAVKRIIGE 250

186 GLAAGVAVILKOLMPOIKVIAVEADSAICKALDGHPRVDFAGVAVKRIIGE 245

251 TFRLOEYLDITITVDSDAICAMKDLFEDVRAVAPSGALALAGMKVYALANIGERL 310

246 TFRLOEYLDITITVDSDAICAMKDLFEDVRAVAPSGALALAGMKVYALANIGERL 305

311 AHLISGANVPHGLRVSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 370

306 IAVTSGANVPHGLRVSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 365

371 FAANAKACITVGRVLSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 430

366 YGDERKATITVGRVLSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 424

431 LOERLYSFEPPSPGAKLRFPLNTLGTWNISLFHRSHTGYRVLAAPKGDH--PDPE 489

425 ENERLYSFEPPSPGAKLRFPLNTLGTWNISLFHRSHTGYRVLAAPKGDH--PDPE 484

490 TRINELGYDCHDETNNPAFRPFLA 513

485 GFLESIGSYHEETONAAVYKFLA 508

RESULT 11

E75502

theonine ammonia-lyase (EC 4.3.1.19) DR0567 [similarity] - *Deinococcus radiodurans* (str

C) Species: *Deinococcus radiodurans*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jun-2002

C/Accession: E75502

R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: E75502

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-568 <WHI>

A/Cross-references: GB:AE001915; GB:AE00513; NID:96458262; PIDN:AAF10147.1; PID:9645826

A/Experimental source: strain R1

C/Genetics:

A/Genes: DR0567

A/Map position: 1

C/Suprafamily: theonine dehydratase

C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos

F;116/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 52.4%; Score 1380.5; DB 2; Length 568;

Best Local Similarity 53.8%; Pred. No. 7e-89;

Matches 276; Conservative 92; Mismatches 134; Indels 11; Gaps 4;

6 PLSGAPEGAELVLRAPVYEAQVTPLOKMEKLSRLDNVILVKREDROPVHSFKRG 65

60 PLPGLDMDVLRALTSQVGAATETPLSPAPRHSRSGNRVLLKREDQDPIFSFKRG 119

66 AYAMAGLITEQKAGHGVITTAAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGFG 125

120 AYNKASQLSAEBRAGVIVCASAGNHAQVAFSSARLGVKALIMPTATADIKVDAVVRGFG 179

126 GEVILHGNFDEAKKATELSQOQGFVTPPDHVPVIAAGGTTALELLODAHLN--RVF 184

180 AEVILHGSFSDAEFALALQERGLTVHPDDPVDVIAAGGTTALELLODAHLN--RVF 239

185 VEVGGGGLAAGVAVILKOLMPOIKVIAVEADSAICKALDGHPRVDFAGVAVKRIIGE 244

240 VEVGGGGLAAGVAVILKOLMPOIKVIAVEADSAICKALDGHPRVDFAGVAVKRIIGE 299

245 KRIGETFRLOEYLDITITVDSDAICAMKDLFEDVRAVAPSGALALAGMKVYALANIGERL 304

300 KQGVATFEDLTRVYDDWVRVTDVCAIKVDPDTRAVIEPAGALSVAGIKKYAAATHG 359

305 IGERLHILSGANVPHGLRVSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 364

360 IHDRTVALTGCANINPRLRVAERTIEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 419

365 TEFNRFADAKNACITVGRVLSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 424

420 TEFNRFADAKNACITVGRVLSRCEGEORALLAVTIPKSGFLKFCOLLGSGVTEPNR 478

425 GRPSPHLOERLYSFEPPSPGAKLRFPLNTLGTWNISLFHRSHTGYRVLAAPKGDH--PDPE 484

479 GRAPRAVERVYAFVFFPERPGALHDFLTOLQENWISLFHRSHTGYRVLAAPKGDH--PDPE 535

485 EBD-----FETRLNELGYDCHDETNNPAFRPFLA 512

536 -PDAAITRFPGFLAGLGPADHVTSPAYRFLA 567

RESULT 12

R83603

theonine dehydratase, biosynthetic PA0331 [imported] - *Pseudomonas aeruginosa* (strain P

C) Species: *Pseudomonas aeruginosa*

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Jun-2002

C/Accession: R83603

R/Stover, C.K.; Ham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lartig, K.; Lam,

., Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: F83603
 A/Status: preliminary
 A/Molecule-type: DNA
 A/Residues: 1-504 <STO>
 A/Cross-references: GB:AE004471, GB:AE004091, NID:99946176, PIDN:AA003720.1, GSPDB:GN001
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: 11val; PA0331
 C/Superfamily: threonine dehydratase

Query Match 51.4%; Score 1354; DB 2; Length 504;
 Best Local Similarity 52.6%; Pred. No. 4.3e-87;
 Matches 263; Conservative 95; Mismatches 140; Indels 2; Gaps 2;

Oy 15 EYLRAVLRAPYEAQVTPLOKMEKLSRLDNVILVREKROPVHSEFKLRGAYMMAGLT 74
 Db 4 QYVKILTSRYDYAVETPQPARQLSERLGNQVILKREDLPFPSEFKIRAKYKVAQLT 63
 Oy 75 EEOKAHGVITASAGNHAQGVAFSSARLGVKALVMPATADIKYDAVRGFGVEVLLHGAN 134
 Db 64 EEEKARGVITASAGNHAQGVAFSSARLGVKALVMPATADIKYDAVRGFGVEVLLHGDA 123
 Oy 135 FDEAKAIEISQOQGFVWPPFDPHVMVIAQGTIALELL-QODAHDRVFPVGGGGLA 193
 Db 124 FPEALHAHLKLVDEKGYTFVHPYDDPDTIAGQGVAMEILRQGPRLDAIFVPVGGGLV 183
 Oy 194 AGVAVLILKOLMPOIKVIAVEADSDACKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFR 253
 Db 184 AGIAVAVKRLRPEIKIIGVEPDESNCLOAANAAGRRVVLGGVGFADVAQAQIGQHTFD 243
 Oy 254 LCOEYLDITITVSDAICAMKDLFEDVRAVAEPPSALALAGMKKYIALHNIRGERLAHI 313
 Db 244 ICKHVDVEIVTSDEICAIKIDYDTRSTTERGALAAVAGIKKYVREBAEQITLVAI 303
 Oy 314 LSGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 373
 Db 304 DSGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCCEAVKRGQITTEFNRYHS 363
 Oy 374 AKNACIFGVRLSGLEERKEILQMLNDGYSVVDLSDEMAKLVHVMNGGRSHLOE 433
 Db 364 GSEAHIFGVQTHPNDRELVAVLREKGFVLDLTNELAKHIRMVGSHAVKVSDE 423
 Oy 434 RLVSFEPPESPGAKLRLFLNTLGTWNISLFYRSHGTDYGVLAFAEXGDHEPD-FETRL 492
 Db 424 MVFFPEPFRERBGLFNFILTKGGRNNISMFHYRNHGADGVVAGLQVPEDEBRLHLPQL 483
 Oy 493 NELGYDCHDETNNPAFRFLL 512
 Db 484 EAIGYPYWDETANPAYQLFL 503

RESULT 13

Ai2334
 threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Nostoc sp. (strain PCC 7120)
 C/Species: Nostoc sp. PCC 7120
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C/Accession: AI2334
 R/Kanezo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchih
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A/Accession: AI2334
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-503 <KUD>
 A/Cross-references: GB:BA000019; PIDN:BA075931.1; PID:917133367; GSPDB:GN00179
 C/Genetics:
 A/Gene: atx232
 C/Superfamily: threonine dehydratase
 C/Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 50.1%; Score 1318.5; DB 2; Length 503;
 Best Local Similarity 50.2%; Pred. No. 1.3e-84;
 Matches 251; Conservative 106; Mismatches 140; Indels 3; Gaps 3;

Oy 15 EYLRAVLRAPYEAQVTPLOKMEKLSRLDNVILVREKROPVHSEFKLRGAYMMAGLT 74
 Db 4 DYLVQILTLARVYDYAQSPLAEVAPNISARLNNKLLKREDMQSVFSFKLRGAYKMNLP 63
 Oy 75 EEOKAHGVITASAGNHAQGVAFSSARLGVKALVMPATADIKYDAVRGFGVEVLLHGAN 134
 Db 64 PDLLAQGVITASAGNHAQGVAFSSARLGVKALVMPATADIKYDAVRGFGVEVLLHGD 123
 Oy 135 FDEAKAIEISQOQGFVWPPFDPHVMVIAQGTIALELL-QODAHDRVFPVGGGGLA 193
 Db 124 YDDAIAARQLEAEKGLTFHPDDPVVIAQGTIGMEILRQYQPFHAIFAVGGGLI 183
 Oy 194 AGVAVLILKOLMPOIKVIAVEADSDACKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFR 253
 Db 184 SGIAVAVKRLRPEIKIIGVEPVDADANQSLQGKRVRLSQVGLFADGVAVREVGEETFR 243
 Oy 254 LCOEYLDITITVSDAICAMKDLFEDVRAVAEPPSALALAGMKKYIALHNIRGERLAHI 313
 Db 244 LCOEYVDEIILVDTDDCAAIKQVFEEDTRSLERAGALAAAGAAVVEREQIGQTLVAV 303
 Oy 314 LSGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 373
 Db 304 ACGANVPHGRVYSECELBORREALIATVITPEKGSFLKFCOLLGSRVTEFNYPAD 363
 Oy 374 AKNACIFGVRLSGLEERKEILQMLNDGYSVVDLSDEMAKLVHVMNGGRSHLOE 433
 Db 364 EKLIHIFIGMQL-QNRADKIHVETFAEGFEILDLDLTKLHLHNGHPLAHNE 422
 Oy 434 RLVSFEPPESPGAKLRLFLNTLGTWNISLFYRSHGTDYGVLAFAEXGDHE-PDETR 492
 Db 423 LTVRFEPPESPGALMKVASMSPWNISMFHYRNHGSDYRIVVMQVPEEMEQAF 482
 Oy 493 NELGYDCHDETNNPAFRFLL 512
 Db 483 DSGYQYWDSDNPAYQLFL 502

RESULT 14

S7759
 threonine ammonia-lyase (EC 4.3.1.19) - Synechocystis sp. (strain PCC 6803)
 N/Alternate names: L-threonine deaminase; protein slr2072
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jun-2002
 R/Kanezo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamiizu, E.; Nakamura, Y.; Miyajima, N.;
 o, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S7759
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-508 <KBN>
 A/Cross-references: EMBL:D90905; GB:AB001339; NID:91652360; PIDN:BA17406.1; PID:9165248
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Genetics:
 A/Gene: 11VA
 C/Superfamily: threonine dehydratase
 C/Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos
 F;51/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted
 Query Match 49.6%; Score 1306; DB 2; Length 508;
 Best Local Similarity 50.7%; Pred. No. 9.9e-84;
 Matches 256; Conservative 96; Mismatches 145; Indels 8; Gaps 4;
 Oy 15 EYLRAVLRAPYEAQVTPLOKMEKLSRLDNVILVREKROPVHSEFKLRGAYMMAGLT 74

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 15:27:16 ; Search time 21 Seconds
(without alignments)
1035.609 Million cell updates/sec

Title: NP418220

Perfect score: 2633
Sequence: 1 MADSQLSGAPGEGAYLRAY.....LYGVDCHDETNNPAPRFLAG 514

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1419	53.9	677	4	US-09-252-991A-22442
2	1345	51.1	524	4	US-09-252-991A-27763
3	1277.5	48.5	520	4	US-09-328-352-7451
4	612	23.2	441	1	US-08-403-866-10
5	583.5	22.2	424	1	US-09-134-001C-3876
6	556	21.1	436	3	US-08-669-378-4
7	551	20.9	436	3	US-08-669-378-2
8	550	20.9	411	4	US-09-328-352-5207
9	549	20.9	436	3	US-08-669-378-10
10	549	20.9	436	3	US-08-669-378-12
11	546	20.7	436	3	US-08-669-378-8
12	541	20.5	436	3	US-08-669-378-6
13	512	19.4	374	4	US-09-252-991A-31294
14	449.5	17.1	328	4	US-09-328-352-4536
15	357	13.6	340	4	US-09-789-330A-2
16	355	13.5	331	4	US-09-252-991A-29393
17	337.5	12.8	329	4	US-09-843-297-2
18	326.5	12.4	325	3	US-09-088-435-1
19	275.5	10.5	378	4	US-09-789-330A-4
20	211	8.0	367	4	US-09-134-001C-4168
21	205.5	7.8	319	4	US-09-134-001C-3330
22	204.5	7.8	312	4	US-09-134-001C-3920
23	191.5	7.3	461	4	US-09-328-352-5878
24	173.5	6.6	309	4	US-09-724-623-72
25	165	6.3	308	4	US-09-107-532A-3925
26	163	6.2	551	1	US-08-120-960-2
27	163	6.2	551	4	US-09-347-878-9

28	161.5	6.1	403	4	US-09-328-352-5461	Sequence 5461, Ap
29	159	6.0	307	4	US-09-328-352-8179	Sequence 8179, Ap
30	152	5.8	311	4	US-09-252-991A-25027	Sequence 25027, A
31	150	5.7	748	4	US-09-252-991A-31491	Sequence 31491, A
32	148.5	5.6	382	4	US-09-252-991A-29566	Sequence 29566, A
33	147	5.6	378	4	US-08-311-731A-161	Sequence 161, App
34	143.5	5.5	308	4	US-09-107-532A-6629	Sequence 6629, Ap
35	142	5.4	478	4	US-09-252-991A-16935	Sequence 16935, A
36	140	5.3	335	4	US-09-328-352-5450	Sequence 5450, Ap
37	124.5	4.7	424	4	US-08-311-731A-220	Sequence 220, App
38	121.5	4.6	397	1	US-07-956-697B-5	Sequence 5, Appli
39	121.5	4.6	397	1	US-08-263-098-5	Sequence 5, Appli
40	120.5	4.6	423	4	US-09-328-352-5224	Sequence 5224, Ap
41	119.5	4.5	389	4	US-09-594-193-8	Sequence 8, Appli
42	116	4.4	937	4	US-09-252-991A-32336	Sequence 32336, A
43	115	4.4	612	4	US-09-252-991A-17844	Sequence 17844, A
44	112.5	4.3	443	4	US-09-594-193-9	Sequence 9, Appli
45	110.5	4.2	313	4	US-09-252-991A-28686	Sequence 28686, A

ALIGNMENTS

RESULT 1
US-09-252-991A-22442
Sequence 22442, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22442
LENGTH: 677
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22442

Query Match 53.9%; Score 1419; DB 4; Length 677;
Best Local Similarity 54.4%; Pred. No. 3.5e-132;
Matches 280; Conservative 94; Mismatches 133; Indels 8; Gaps 3;

QY 5 OPLSGA-----PGAEYLRAVLRAFYEAQVTPLOKMEKLSRLDVIIVKREDROPV 58
DB 161 QPMSTSLASAKPLLAGVSEILAAIPYDAVETPLQAPOLSOURLKRVLUKEDLOPV 220
QY 59 HSPFLRGAVYAMAGLTEROKAHGVITASAGNHAQGVAFSSARLGVKALIMPTATADIKV 118
DB 221 PSFKIRGAVYVARLSDQKRGVITTSAGNHAQGLAAARLGVRAVIYVPRTPPELKV 280
QY 119 DAVRFGGEVILHGANPBEAKAKAIELSQOQGFVWPFPDHPMYTAGGTLAELLOQ-D 177
DB 281 KGVLAIRGGEALHGAFFDALAHALQLAERGMFVPPYDPDVAAGGTVAAMELTRHGS 340
QY 178 AHLRVFVPPVGGGGLAAGVAVLIRKQMPQIVIAVEADSACTKALAGHPVDLPRGL 237
DB 341 GRLDATFVPPVGGSLIAGIAYVYKRLRDIIVIGVEPDSKCLQALAAGERVILGQGL 400
QY 238 FAEQVAVRRIGDETFRLCOEYLDIITVSDPAICAMKDLFEDYRAVAEPGATLAAGMK 297
DB 401 FADGAVAAQIACNPFVCKHVDVITVGSDEICAIKDIYDDRSITPEPAGALAVAGIX 460
QY 298 KYIALHNIRGRLAHIIISGANVNHGLRYVEERCELGQRALALAVTIPKSGSLKXCO 357
DB 461 KYVARERTGOTLVALDSGANINFDRLHVAERALEGBREARLAIYVAERPSFKACA 520

APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,866
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 20747/30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1487
TELEFAX: (716) 263-1600
TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp. lactis
INDIVIDUAL ISOLATE: ILVA
US-08-403-866-10

Query Match 23.2%; Score 612; DB 1; Length 441;
Best Local Similarity 37.2%; Pred. No. 3.2e-52;
Matches 143; Conservative 74; Mismatches 151; Indels 16; Gaps 8;
QY 16 YLRVAVLRAPVY--EAAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLRGAYAMAGL 73
DB 28 YLSNRYQANVLYKEVYVTKPLQDPLYSNKYQANTYLEENLQKVRSLKGAAYTSISKL 87
QY 74 TEOKAHGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVAVRGFG--EVLHG 132
DB 88 SDEGRSKVNCASAGNHAGVAFANQINISITIMPPTINQKISQVKGFGESVITRL 147
QY 131 HGANFDEAKAKAIEISQOQGFVWPFPDPHVPVYAGGTALAEELQ---QDAHLDRVVP 186
DB 148 IGDTFDESARAKAFSQNDKRFIDPFDDENVIAQGTVALEIFPAQAKKGISLDRIFVQ 207
QY 187 VGGGGLAGVAVLTKQMPQIKVIAVEADSACTKAALDAGHPVLPVGLFAEGVAVKR 246
DB 208 IGGGGLAGVAVLTKQMPQIKVIAVEADSACTKAALDAGHPVLPVGLFAEGVAVKR 246
QY 247 IGDTEFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEBSGALALAGMKKYIALHNIR 306
DB 268 VQKTYQVILNKVQLAVDEGLISQTLLEYSKGIYAERGAISVALLE--LIKDEIK 325
QY 307 GERLAHLISGANVNFHGLRYVSERCELBQREALLAVTIPERKGSFLKFC--QLLGR--GSV 364
DB 326 GKNIVCIISGNGNDISRMQIEIERALVYEGLGHYFVINPQPGSLRFTVSDILGPNDDI 385
QY 365 TEENY--RFADAKNACIFVGVALS 386
DB 386 TRFEYIKRADKGGKPCCL--VGIIILS 408

RESULT 5
US-09-134-001C-3876
Sequence 3876, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3876
LENGTH: 424
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3876

Query Match 22.2%; Score 583.5; DB 4; Length 424;
Best Local Similarity 34.8%; Pred. No. 2e-49;
Matches 137; Conservative 89; Mismatches 145; Indels 23; Gaps 10;
QY 16 YLRVAVLRAPVYEAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLRGAYAMAGL 75
DB 18 YLR--LKNIVK---TPLOPDHLSQKYNQNVILKEDLQWVRSFKLRGAYMAISVLSN 71
QY 76 EOKAHGVITASAGNHAQGVAFSSARLGVKALIVPTATADIKVAVRGFG--EVLHG 132
DB 72 EKKKGITCASAGNHAGVAVTAKKLNKAVIFMPVTPRQKINQVKGFGDSNVEIYLIG 131
QY 133 ANFDEAKAKAIEISQOQGFVWPFPDPHVPVYAGGTALAEELQ---DAHLDRVVPV 188
DB 132 DTFPHCLAQALNLYKQKRMNFDIPNNVYITAGGTAKELINQAEKEDTFDVYFAIG 191
QY 189 VGGGGLAGVAVLTKQMPQIKVIAVEADSACTKAALDAGHP--VDLPVGLFAEGVAVKR 247
DB 192 GGLISGVSTYFKHSPHTKILGVEPTGASMTQSVINHSITVLENIDKRVDSAVARV 251
QY 248 GDETFRLCOEYLDITVDSDAICAMKDLFEDVRAVAEBSGALALAGMKKYIALHNIR 307
DB 252 GDITFDIAKQVDVYQVDEGAVCSITLDWYSKQAIYAERGAISVALLEQ--KKQIEN 309
QY 308 ERLAHLISGANVNFHGLRYVSERCELBQREALLAVTIPERKGSFLKFC--QLLGR--SVT 365
DB 310 KTVICVIGSGNGNDINRMKQIEIERSLLEEMHYFVILNFPQPGALREFVDVLPQDDIT 369
QY 366 EENYRFADAKN--ACIFGVRLRSLERKEILQM 398
DB 370 KFEYIKRITSQNTGTVIGIQ---LKHDDLIQL 399

RESULT 6
US-08-669-378-4
Sequence 4, Application US/08669378
Patent No. 6107063
GENERAL INFORMATION:
APPLICANT: Moeckel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF
TITLE OF INVENTION: MICROBIAL MICROORGANISMS WITH DEREGULATED TREONINE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 5207
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-5207

Query Match 20.9%; Score 550; DB 4; Length 411;
 Best Local Similarity 35.2%; Pred. No. 4,2e-46;
 Matches 134; Conservative 79; Mismatches 158; Indels 10; Gaps 6;

QY 32 TPLQMKETLSRLDNVILVKREDROPVHSFKLRGAYMMAGITTEOKAHGYTTASAGNHA 91
 DB 30 TPFVSEITISKTLGKMKLKFENLQFTASFKEGKALNLTLSSEKQHGVIASAGNHA 89
 QY 92 QGVAFSSARLVKALIVPTATADIKVDVARGFGEVLLHGANFDEAKAKIELSQOQGF 151
 DB 90 QGVAYHAQRTGVATITVMPKSTPNVKQVRVEYGARVILHGQDFSEAAAEHMRVAQESL 149
 QY 152 TWVPEPDHPVIAAGGTALTELQODAHLDVFPVPGGGIAGAVAVLIKOLMPOIKYA 211
 DB 150 TIIFPDAAELIAGGTLALEMLVDPDLIVPDIIGGGILSGIAIAKTIINPKIKITG 209
 QY 212 VEADSDACKLALADAGHPVDLPRVGLPAEGVAVKRIQDETFRLCOEYLDIITVDSDAIC 271
 DB 210 VQSVVYPSM-AKLICNVGLAVSMGSTVAEGIAVTKPGLTTQIAKHFPVDIIVVTEMDIE 268
 QY 272 AAMQDLFEDVAVAPSPGALLAGKKTIALHNIRGEHLAHLISGANVFGLRYVSERC 331
 DB 269 EAILLNIEKTVCEGAGATGIAAIMSRPD--FLGHKVGAVLISGNDITFVWVSVLQRH 326
 QY 332 ELGROREALVTTIPEEKGSFLKFCQLG--GRSVTEFNY-RFA--DAKNACIFVGVL 385
 DB 327 LTRGRMWRIVELPDNGALARLTALTAEGCGNIYELRHAFATSPAKESAVSDIEL 386
 QY 386 SRGLEERKEILQMLNDGYSV 406
 DB 387 -KSAPDLEPLIQAMQLEGYIV 406

RESULT 9
 US-08-669-378-10
 Sequence 10, Application US/08669378
 Patent No. 6107063
 GENERAL INFORMATION:
 APPLICANT: Moeckel, Bettina
 APPLICANT: Eggeling, Lothar
 APPLICANT: Sahm, Hermann
 TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF
 TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE
 TITLE OF INVENTION: DEHYDRATASE
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESS: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,378
 FILING DATE: 20-MAR-1997

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DE95/00017
 FILING DATE: 09-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 00 926.7
 FILING DATE: 14-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Bent, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 016881/0142
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-669-378-10

Query Match 20.9%; Score 549; DB 3; Length 436;
 Best Local Similarity 35.6%; Pred. No. 5,8e-46;
 Matches 144; Conservative 73; Mismatches 160; Indels 28; Gaps 12;

QY 13 GAETLRA---VLNAPYEAQVTPLOMKETLSRLDNVILVKREDROPVHSFKLRGAYA 68
 DB 17 GAELIRADIOTQARISSVIAFPPLQYCPRLSEETGAETILKREDIDQDVASYIKGLN 76
 QY 69 MMAGLTEROKAHGYTTASAGNHAQVAFSSARLVKALIVPTATADIKVDVARGFGE- 127
 DB 77 SGAOSPOGRDAGVLAASAGNHAQVAVYCKSLGQRTIVPVOTPKOKRPRIMWGGEEF 136
 QY 128 --VLLHGANFDEAKAKIELSQOQGFVWPEPDHPVIAAGGTALTELQODAHLDVFPV 181
 DB 137 VSLVVTGNPNDEASAAAHEDERTGATLIBEPDARNVIGGTVAAILSLQTSMGKAD 196
 QY 182 RVFPVPGGGIAGAVAVLIKOLMPOIKYIAVEADSDACKLALADAGHPVDLPRVGLPAEG 241
 DB 197 HWVPVPGGGIAGAVAVYMAEMAPRTAIVGIEPAGAASMQAALHANGGFTLETVDPFVDG 256
 QY 242 VAVKRIQDETFRLCOEYLDI--ITVDSDAICAMQDLFEDVAVAPSPGALLAGKKTIAL 299
 DB 257 AEVRVQDLNNTIYVKQGRVHMSATGAVCTEMLDLYOEGITAEPAAGALSTAGLKE- 315
 QY 300 IALHNIRGERLAHLISGANVFHGLRY--VSERCLEGEORBALAVTIPEEKGSFLKFCQ 357
 DB 316 --NSFADGSVVVCIISGNDV--LRYAEIAERSLVHRGLKHYFLVNFPOKPRQLRHLE 371
 QY 358 -LIG-GRSVTEFNY-RPADAKNACIFVGVLRS--GLE--ERKE 394
 DB 372 DILPDPDITLTFEYLKENNETGTALVGHILHSEASGLDSLRLERME 416

RESULT 10
 US-08-669-378-12
 Sequence 12, Application US/08669378
 Patent No. 6107063
 GENERAL INFORMATION:
 APPLICANT: Moeckel, Bettina
 APPLICANT: Eggeling, Lothar
 APPLICANT: Sahm, Hermann
 TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF
 TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE
 TITLE OF INVENTION: DEHYDRATASE
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESS: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,378
FILING DATE: 20-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 0166881/0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
JS-08-669-378-12

Db 372 DILGPDDITLCEYLKNNRETGTALVGIHLSEASGLDILLERNE 416

RESULT 12

US-08-669-378-6

Sequence 6, Application US/08669378

Patent No. 610763

GENERAL INFORMATION:

APPLICANT: Moeckel, Bettina

APPLICANT: Eggeling, Lothar

APPLICANT: Sahn, Hermann

TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF

TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE

NUMBER OF INVENTION: DEHYDRATASE

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/669,378

FILING DATE: 20-MAR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DE95/00017

FILING DATE: 09-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 00 926.7

FILING DATE: 14-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 016881/0142

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 436 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-669-378-6

Query Match 20.5%; Score 541; DB 3; Length 436;

Best Local Similarity 35.3%; Pred. No. 3.6e-45;

Matches 143; Conservative 73; Mismatches 161; Indels 28; Gaps 12;

Db 13 GAEYLR-----VLRAPYEAQVTPLOKMEKLSRLDNVILVKEEDROPVHSEFLKRAYA 68

Db 17 GAEIRADIGTAAARISVIAFPPLQYCPRLSEETGAELYLKREDDQVRSYKIRALN 76

Db 69 MMALGTEOKAHGIVITASAGNHAQVAFSSARLGKALIVPTATADIKYDAVAFSGE- 127

Db 77 SGASPOEORDAGIVAASAGNHAQVAVCKSLGVQGRIVYVPTPKOKDRIVHGGEE 136

Db 128 --VLLHGANDEAKAKAIELSQOQFTWPPDPHVMVIAQGTALALELLQDAHL---D 181

Db 137 VSLVVTGNNFDEAASAAHEDERTGATLIBPFDARNTVIGGTVAAEILISQLTSMGSAD 196

Db 182 RVFVPGGGGLAAAVAVILKLMQIKIVANVADSAICRAALNAGHPVLLPRGLPAEG 241

Db 197 HWVPVGGGGLAGVAVSMAMARITVIGIEPAGAAQMALHNGPITLETVDPEVDG 256

Qy 242 VAVRIGDETFRICOEYLDI--ITVDSDAICAMKDLFEDVAVAPSSGALALAGMKY 299

Db 257 AEYKRVGDLNVTIVKKNQGRVHMMASATGAVCTEMDLVNEGILAPAPALAGLKE- 315

Qy 300 IALHNIRGERLAIILSGANVNFHGLRY--VSECEIGEOREALLAVTIPEKSGFLKFCQ 357

Db 316 --MSFAPGSVVVCCISGGNNDV--LRYAEIERSLVHGHKHYFLVFPQKPOLRHFLE 371

Qy 358 -LIG-GRSVTEFNY-RRADKAKACIFGVRLSR--GLE---ERKE 394

Db 372 DILGPDDITLCEYLKNNRETGTALVGIHLSEASGLDILLERNE 416

RESULT 13

US-09-252-991A-31294

Sequence 31294, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31294

LENGTH: 374

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31294

Query Match 19.4%; Score 512; DB 4; Length 374;

Best Local Similarity 32.5%; Pred. No. 2.2e-42;

Matches 119; Conservative 67; Mismatches 134; Indels 46; Gaps 5;

Qy 7 LSGAPGAEYLRVLAPEY-----AAQV-----TPLOKMEKLSRLDNVILVKEEDR 55

Db 44 LSSLPSSEPTWMDL--PTVDVIAAARIGHANRPVWSSRTLDELGAEVFFKCNL 101

Qy 56 QPVHSEFLKRAYAMMAGLTSEOKAHGIVITASAGNHAQVAFSSARLGKALIVPTATAD 115

Db 102 QRMGAFFERGAFAALSRFSABQRAAGVAFSSGNHQAIALSARLIGIPPTIWPADAPA 161

Qy 116 IKYDAVAFSGEYVLLHGANDEAKAKAIELSQOQFTWPPDPHVMVIAQGTALALELLQ 175

Db 162 VKIEATRGYGQVVLVDRTYEDBEQIGRLAQHGLTILPPYDHPVLAQGRPAKELFE 221

Qy 176 QDAHLDRVFPVGGGGLAGVAVILKLMQIKIVANVADSAICRAALNAGHPVLLPRV 235

Db 222 EVGPLDAFFAPLGGGGLISGCLALIRALAPACRIYGVPEAGNDGQSLSGAIVHIDTP 281

Qy 236 GLAEGYAVARRIDETFRLCQEVLDIITVDSDAICAMKDLFEDVAVAPSSGALALAG 295

Db 282 QTLADGQTOHLNLTFFPLQRVNVDILTASDAELVDGKFLAARMKLIVEPTGCLGLAA 341

Qy 296 MKKYIALHNIRGERLAIILSGANVNFHGLRYVSECEIGEOREALLAVTIPEKSGFLK 355

Db 342 ARQ--RKDELKRGKRVGLISGNID-----LARF 368

Qy 356 COLLGG 361

Db 369 CALLGG 374

RESULT 14

US-09-328-352-4536

Sequence 4536, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: PATENT FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4536
LENGTH: 328
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4536

Query Match 17.1%; Score 449.5; DB 4; Length 328;
Best Local Similarity 34.4%; Pred. No. 2,9e-36;
Matches 107; Conservative 58; Mismatches 133; Indels 13; Gaps 3;

QY 21 LRAPYVE---AAQ-----VTPLQKMEKLSRLDNVILVREDRQPVHSFKLGAYAM 69
DB 10 LRLPNVEDVAAAERIKDFINKTPTVLTSTVNNNEFAEVEFFKCNFQVGAFFKFGAMNA 69
QY 70 MAGLIEBQAHGVITTSAGNAGVAFSSARLGKALVIMPTATADIKVDVARGGCVL 129
DB 70 LQFNETQKAGVAFSSGNHQAALSSKILGIPATIIIPKDPAPAKMAATREYGGNTV 129
QY 130 LHGANDEAKAKAIELSSQOGFTVPFPDHPVVIAGGTLALELQDAHLDRVFPVVG 189
DB 130 EEDRYTEDEKIKETAEKNGLLTLPSPHYIAGGTAKELFEVGDLDLFLVCLGG 189
QY 190 GGLAGVAVAILKQMLQIVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRI 249
DB 190 GGLAGSALSARQLSPKCIYGEVPALGNDGWSFRKGEIVHIDPTIADGQTYLGK 249
QY 250 ETPRLCOEYLDITITDSALICAMKDLFEDVRAVAEBSGALALAGMKYIALHNI 309
DB 250 LTFPIIQOQVDDILTVTDEILNAMKFAERMKVVEPTGCLGFAAARN--LKDILKGR 307
QY 310 LAHISGANVN 320
DB 308 IGIISGANVD 318

RESULT 15
US-09-789-300A-2
Sequence 2, Application US/09789300A
Patent No. 6438576
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
FILE REFERENCE: Dependent Enzyme Family Member and Uses Therefore
CURRENT APPLICATION NUMBER: US/09/789,300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-789-300A-2

Query Match 13.6%; Score 357; DB 4; Length 340;
Best Local Similarity 30.7%; Pred. No. 4.8e-27;
Matches 93; Conservative 66; Mismatches 134; Indels 10; Gaps 5;

QY 25 VTEAAQVTPLOKMEKLSRLDNVILVREDRQPVHSFKLGAYAMAGLTE---EOKAHG 81
DB 19 IRDSIHLLTPTSSILQLTGRNLFKCELFQKTSFKIRGALNAVASLVPDALERKPKA 78
QY 82 VITASAGNHAGVAFSSARLGKALVIMPTATADIKVDVARGGCVLHGANFDEAKAK 141

DB 79 VVTHSSGNHGALTYAAKLEIGIPYIVPQTPAPDCKLALQAYASIVCEPSDSRENV 138
QY 142 AIESSQOOGFTWVPFPDHPVVIAGGTLALELQDAHLDRVFPVGGGGLAGVAVLIK 201
DB 139 AKRYTEETEGIMVHPNCEPAVIAOGGTLALEVNOVPLVDALVVPVGGGMLAGIATVK 198
QY 202 QLMPOIKYIAVE---AEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIQDETRLCOEY 258
DB 199 ALKPSVKYVAEBSNADD--CYQSKLKGKMLPNLYPPTIADGVK--SSIGLNTWPIIRDL 255
QY 259 LDDITVDSALICAMKDLFEDVRAVAEBSGALALAG--MKYIALHNIHGERLAHISGA 317
DB 256 VDDIFTVEDEIKCATQLWERMKLLIPTAGVAAVLSQHFTQVSEPVKNICIVLSGG 315
QY 318 NVN 320
DB 316 NVD 318

Search completed: December 18, 2003, 15:30:48
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 15:27:16 ; Search time 39 seconds

(without alignments)
3401.001 Million cell updates/sec

Title: NP418220

Sequence: 1 MADSGPLSGAPEGAYLRV.....LGYDCHDETNNPAPRFLAG 514

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

SPTREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_ornithine: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2622	99.6	514	16	Q8X318
2	2615	99.3	515	16	Q8FBR4
3	2575.5	97.8	515	16	Q8X467
4	2520	95.7	514	16	Q8Z378
5	2249	85.4	514	16	Q8ZAR4
6	1888.5	71.7	509	16	Q8DDG2
7	1849.5	70.2	510	16	Q8KVM1
8	1550	58.9	545	16	Q8E9B0
9	1415.5	53.8	515	16	Q91418
10	1410.5	53.6	508	16	Q9JUX5
11	1400.5	53.2	508	16	Q9JZM1
12	1380.5	52.4	568	16	Q9RMU8
13	1354	51.4	504	16	Q916G0
14	1318.5	50.1	503	16	Q8YPG2
15	1307.5	49.7	507	16	Q8Y287
16	1306	49.6	508	16	P73375

17	1180.5	44.8	602	10	Q8W314	Q8W314 oryza sativ
18	1123.5	42.7	600	3	Q94634	Q94634 schizosacch
19	1123	42.7	602	10	Q9AU01	Q9AU01 oryza sativ
20	1094.5	41.6	601	10	Q9AXU4	Q9AXU4 nicotiana a
21	1088	41.3	592	10	Q8GUG5	Q8GUG5 arabidopsis
22	880.5	33.4	404	2	Q9F770	Q9F770 uncultured
23	612.5	23.3	406	16	Q8DW42	Q8DW42 streptococ
24	610	23.2	404	16	Q8RDT9	Q8RDT9 fusobacteri
25	603.5	22.9	415	16	Q8G466	Q8G466 bifidobacte
26	601	22.8	420	2	Q9XB12	Q9XB12 bacillus ce
27	597	22.7	422	16	Q8NV18	Q8NV18 staphylococ
28	594	22.6	422	16	Q9SEJ1	Q9SEJ1 staphylococ
29	593	22.5	409	16	Q9EWG3	Q9EWG3 streptococ
30	590.5	22.4	422	16	Q8Y5R5	Q8Y5R5 listeria mo
31	583.5	22.2	424	16	Q8CNK9	Q8CNK9 staphylococ
32	580.5	22.0	416	16	Q97SD4	Q97SD4 streptococ
33	580.5	22.0	416	16	Q8DR02	Q8DR02 streptococ
34	579.5	22.0	402	16	Q8XL77	Q8XL77 clostridium
35	577.5	21.9	422	16	Q92A24	Q92A24 listeria in
36	570.5	21.7	406	17	Q9HLM2	Q9HLM2 thermoplas
37	566	21.5	495	17	Q9HNH6	Q9HNH6 halobacteri
38	558.5	21.2	403	16	Q9PP95	Q9PP95 campylobact
39	556	21.1	401	16	Q9WTJ1	Q9WTJ1 thermotoga
40	554	21.0	370	2	Q9RC71	Q9RC71 bacillus ha
41	551	20.9	419	16	Q8YH69	Q8YH69 brucella me
42	545.5	20.7	436	16	Q8FMW7	Q8FMW7 corynebacte
43	543.5	20.6	405	17	Q97CB2	Q97CB2 thermoplas
44	533	20.2	329	16	Q8ZJX4	Q8ZJX4 salmonella
45	531	20.2	338	16	Q8EN71	Q8EN71 oceanobacill

ALIGNMENTS

RESULT 1
Q8X318 PRELIMINARY; PRT; 514 AA.
ID Q8X318;
AC Q8X318;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Theonine deaminase.
GN ECS4706.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCB1_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231, PubMed=11259796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Mura T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AP002556; BAB38129.1; -;
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydrtase.
DR InterPro; IPR001721; Thrdh_C.
DR InterPro; IPR005787; Thr_dehydratase.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydrat_C; 2.
DR TIGRfam; TIGR01124; llyA_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
SQ SEQUENCE 514 AA; 56184 MW; ACF4692F14FCB85 CRC64;

Query Match 99.6%; Score 2622; DB 16; Length 514;
Best Local Similarity 99.2%; Pred. No. 1.4e-174;
Matches 510; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MADSOPLSGAPGEGAYLRVAVLRAVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
DB 1 MADSOPLSGAPGEGAYLRVAVLRAVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
QY 61 FKLRGAYAMAGLTTEOKAHGVTITASAGNHAOGVAFSSARLGVKALIIMPTATADIKVDA 120
DB 61 FKLRGAYAMAGLTTEOKAHGVTITASAGNHAOGVAFSSARLGVKALIIMPTATADIKVDA 120
QY 121 VRFGEVVLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLALELLQODAH 180
DB 121 VRFGEVVLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLALELLQODAH 180
QY 181 DRFPVVGGGGAGAAVAVILKQMPQIKYIAVEABDSACKALADAGHPVDLPRVGLFAE 240
DB 181 DRFPVVGGGGAGAAVAVILKQMPQIKYIAVEABDSACKALADAGHPVDLPRVGLFAE 240
QY 241 GVAVKRIGDETFRLOCEYLDIIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKKYI 300
DB 241 GVAVKRIGDETFRLOCEYLDIIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKKYI 300
QY 301 ALHNIRGERLAHILSGANVFHGLRYVSERCLEGEOREALLAVTIPEEKGFLEKFCOLLG 360
DB 301 AOHNIRGERLAHILSGANVFHGLRYVSERCLEGEOREALLAVTIPEEKGFLEKFCOLLG 360
QY 361 GRSVTEFNFRPADAKNACIFVGVRLSRGLSEERKEILOMLNDGYSVVDLSDDMAKLHYR 420
DB 361 GRSVTEFNFRPADAKNACIFVGVRLSRGLSEERKEILOMLNDGYSVVDLSDDMAKLHYR 420
QY 421 YWVGSRPSHPLQERLYSEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAARE 480
DB 421 YWVGSRPSHPLQERLYSEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAARE 480
QY 481 XGDHBPDEFTRLNELGYDCHDETNNPAFRFLAG 514
DB 481 XGDHBPDEFTRLNELGYDCHDETNNPAFRFLAG 514

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RESULT 2

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ID Q8FBR4 PRELIMINARY; PRT; 515 AA.
AC Q8FBR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Threonine dehydratase biosynthetic (EC 4.3.1.19).
GN ILVA OR C4694.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
ON NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raske D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016769; AAN8126.1; -.
KW lysase; Complete proteome.
SQ SEQUENCE 515 AA; 56285 MM; AF0777C496585871 CRC64;

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Query Match 99.3%; Score 2615; DB 16; Length 515;
 Best Local Similarity 99.0%; Pred. No. 4,4e-174;
 Matches 509; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MADSOPLSGAPGEGAYLRVAVLRAVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
DB 1 MADSOPLSGAPGEGAYLRVAVLRAVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 60
QY 2 MADSOPLSGAPGEGAYLRVAVLRAVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 61
DB 2 MADSOPLSGAPGEGAYLRVAVLRAVYEAQVTPLOQMEKLSRLDNVILVKREDROPVHS 61

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QY 61 FKLRGAYAMAGLTTEOKAHGVTITASAGNHAOGVAFSSARLGVKALIIMPTATADIKVDA 120
DB 62 FKLRGAYAMAGLTTEOKAHGVTITASAGNHAOGVAFSSARLGVKALIIMPTATADIKVDA 121
QY 121 VRFGEVVLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLALELLQODAH 180
DB 122 VRFGEVVLHGANFDEAKAKAIELSQOQGFVWPFPDHPMVIAGGTLALELLQODAH 181
QY 181 DRFPVVGGGGAGAAVAVILKQMPQIKYIAVEABDSACKALADAGHPVDLPRVGLFAE 240
DB 182 DRFPVVGGGGAGAAVAVILKQMPQIKYIAVEABDSACKALADAGHPVDLPRVGLFAE 241
QY 241 GVAVKRIGDETFRLOCEYLDIIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKKYI 300
DB 242 GVAVKRIGDETFRLOCEYLDIIITVDSDAICAMKDLFEDVRAVAEPGALALAGMKKYI 301
QY 301 ALHNIRGERLAHILSGANVFHGLRYVSERCLEGEOREALLAVTIPEEKGFLEKFCOLLG 360
DB 302 AOHNIRGERLAHILSGANVFHGLRYVSERCLEGEOREALLAVTIPEEKGFLEKFCOLLG 361
QY 361 GRSVTEFNFRPADAKNACIFVGVRLSRGLSEERKEILOMLNDGYSVVDLSDDMAKLHYR 420
DB 362 GRSVTEFNFRPADAKNACIFVGVRLSRGLSEERKEILOMLNDGYSVVDLSDDMAKLHYR 421
QY 421 YWVGSRPSHPLQERLYSEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAARE 480
DB 422 YWVGSRPSHPLQERLYSEFPSPGAXLRFLNTLGTWNISLPHYRSHGTDYGRVLAARE 481
QY 481 XGDHBPDEFTRLNELGYDCHDETNNPAFRFLAG 514
DB 482 XGDHBPDEFTRLNELGYDCHDETNNPAFRFLAG 515

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RESULT 3

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ID Q8X467 PRELIMINARY; PRT; 515 AA.
AC Q8X467;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)
DE Threonine deaminase (Dehydratase).
GN ILVA OR Z5283.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
ON NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:528-533(2001).
DR EMBL; AE005608; AAG58967.1; -.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydrtase.
DR InterPro; IPR001721; ThrDh_C.
DR InterPro; IPR005787; Thr_dehydrataseI.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydrat_C; 2.
DR TIGRFAMs; TIGR01124; ilva_2cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 515 AA; 56339 MM; C57C02BEF717D05F CRC64;

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Query Match 97.8%; Score 2575.5; DB 16; Length 515;
 Best Local Similarity 98.1%; Pred. No. 2.5e-171;
 Matches 505; Conservative 4; Mismatches 5; Indels 1; Gaps 1;


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QY 1 MADSOPLSGAPGAEYLRATLRAPVYEAQVTPLOQKMEKSSRLDNVILVKREEROPVHS 60
DB 1 MADSOPLSGAPGAEYLRATLRAPVYEAQVTPLOQKMEKSSRLDNVILVKREEROPVHS 60
QY 61 FKLKGAAYAMAGLTBEQKAGVITASAGNHAQVAFSSARLGVKALIVMPTATADIKYDA 120
DB 61 FKLKGAAYAMAGLTBEQKAGVITASAGNHAQVAFSSARLGVKALIVMPTATADIKYDA 120
QY 121 VRGFGSVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPVIAQGTLLLELLOQDASHL 180
DB 121 VRGFGSVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPVIAQGTLLLELLOQDASHL 180
QY 181 DRVFPVPGGGGLAAGVAVLIKQIMPQIKVIAVEADSCAKALDAGHPVDLPRVGLFAE 240
DB 181 DRVFPVPGGGGLAAGVAVLIKQIMPQIKVIAVEADSCAKALDAGHPVDLPRVGLFAE 240
QY 241 GVAAYKRIQDETFRICQEYLDIITVDSDAICAMKDLFEDVRAVAEPSGALALAGMKKYI 300
DB 241 GVAAYKRIQDETFRICQEYLDIITVDSDAICAMKDLFEDVRAVAEPSGALALAGMKKYI 300
QY 301 ALHNIRGR-LAHILSGANVNFHGLRYVSERCGEQREALLAVTIPEKGSFLKFCQLL 359
DB 301 AQHNIRMTGVAAHLLSGANVNFHGLRYVSERCGEQREALLAVTIPEKGSFLKFCQLL 360
QY 360 GGRSVTEFNYPADAKNACTIVGVRLSRGLERKEIILQMLNDGGYVVDLSDDDEAKLHV 419
DB 361 GGRSVTEFNYPADAKNACTIVGVRLSRGLERKEIILQMLNDGGYVVDLSDDDEAKLHV 420
QY 420 RYMGGRPSHPLQERLYSFEPSPGAXLRFNLGTWNTSLFHYRSHGTDYGRVLAFAE 479
DB 421 RYMGGRPSHPLQERLYSFEPSPGAXLRFNLGTWNTSLFHYRSHGTDYGRVLAFAE 480
QY 480 EXGHEPDPFETRLNELGYDCHDETNNPAFRFFLAG 514
DB 481 ELGDHEPDPFETRLNELGYDCHDETNNPAFRFFLAG 515

RESULT 4
ID 082378 PRELIMINARY; PRT; 514 AA.
AC 082378;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Threonine deaminase.
GN STY3652.
OS Salmoneilla typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmoneilla.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Baaham D., Brooks K., Chillingworth T., Comerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jajels K.,
RA Krogh A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmoneilla
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627279; CAD09412.1;
DR InterPro; IPR001926; B6 enzyme beta.
DR InterPro; IPR00634; S/F dehydrtase.
DR InterPro; IPR001721; ThDh_C.
DR InterPro; IPR005787; Thr_dehydrtaseI.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydrtat_C; 2.

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DR TIGRFAMs; TIGR01124; i1va_2Cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KM Complete proteome.
SQ SEQUENCE 514 AA; 56276 MW; 17B0E670D66E035B CRC64;

Query Match 95.7%; Score 2520; DB 16; Length 514;
Best Local Similarity 94.9%; Pred. No. 1,9e-167;
Matches 488; Conservative 18; Mismatches 8; Indels 0; Gaps 0;

QY 1 MADSOPLSGAPGAEYLRATLRAPVYEAQVTPLOQKMEKSSRLDNVILVKREEROPVHS 60
DB 1 MADSOPLSGAPGAEYLRATLRAPVYEAQVTPLOQKMEKSSRLDNVILVKREEROPVHS 60
QY 61 FKLKGAAYAMAGLTBEQKAGVITASAGNHAQVAFSSARLGVKALIVMPTATADIKYDA 120
DB 61 FKLKGAAYAMAGLTBEQKAGVITASAGNHAQVAFSSARLGVKALIVMPTATADIKYDA 120
QY 121 VRGFGSVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPVIAQGTLLLELLOQDASHL 180
DB 121 VRGFGSVLLHGANFDEAKAKAIELSQOQGFVWPFPDHPVIAQGTLLLELLOQDASHL 180
QY 181 DRVFPVPGGGGLAAGVAVLIKQIMPQIKVIAVEADSCAKALDAGHPVDLPRVGLFAE 240
DB 181 DRVFPVPGGGGLAAGVAVLIKQIMPQIKVIAVEADSCAKALDAGHPVDLPRVGLFAE 240
QY 241 GVAAYKRIQDETFRICQEYLDIITVDSDAICAMKDLFEDVRAVAEPSGALALAGMKKYI 300
DB 241 GVAAYKRIQDETFRICQEYLDIITVDSDAICAMKDLFEDVRAVAEPSGALALAGMKKYI 300
QY 301 ALHNIRGR-LAHILSGANVNFHGLRYVSERCGEQREALLAVTIPEKGSFLKFCQLL 360
DB 301 AQHNIRMTGVAAHLLSGANVNFHGLRYVSERCGEQREALLAVTIPEKGSFLKFCQLL 360
QY 361 GGRSVTEFNYPADAKNACTIVGVRLSRGLERKEIILQMLNDGGYVVDLSDDDEAKLHV 420
DB 361 GGRSVTEFNYPADAKNACTIVGVRLSRGLERKEIILQMLNDGGYVVDLSDDDEAKLHV 420
QY 421 RYMGGRPSHPLQERLYSFEPSPGAXLRFNLGTWNTSLFHYRSHGTDYGRVLAFAE 480
DB 421 RYMGGRPSHPLQERLYSFEPSPGAXLRFNLGTWNTSLFHYRSHGTDYGRVLAFAE 480
QY 481 XGDHEPDPFETRLNELGYDCHDETNNPAFRFFLAG 514
DB 481 LGDHEPDPFETRLNELGYDCHDETNNPAFRFFLAG 514

RESULT 5
ID 082AB4 PRELIMINARY; PRT; 514 AA.
AC 082AB4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Threonine dehydratase (EC 4.2.1.16) (Threonine deaminase).
GN IIVA OR YPO3896 OR Y0339.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tariga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jajels K., Karlyshev A.V.,
RA Leather S., Moulé S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).

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RP SEQUENCE FROM N.A.
 RC STRAIN-KIMS / Bivovar Mediaevalls;
 RX MEDLINE=22137853; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AJ414159; CAC93363.1; -.
 DR EMBL; AE013634; AAM83930.1; -.
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/T dehydratase.
 DR InterPro; IPR001721; ThrDh C.
 DR InterPro; IPR005787; Thr_dehydratet.
 DR Pfam; PF00291; PALP; 1.
 DR Pfam; PF00585; Thr_dehydrat C; 2.
 DR TRIGRAMS; TRIGR01124; 11VA_2Cterm; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 KM Lyase; Complete proteome.
 SQ SEQUENCE 514 AA; 55935 MW; A49EA796A2CE6640 CRC64;

Query Match 85.4%; Score 2249; DB 16; Length 514;
 Best Local Similarity 84.2%; Pred. No. 1.5e-148;
 Matches 433; Conservative 40; Mismatches 41; Indels 0; Gaps 0;

QY 1 MADSQLSGAPBEAEYLRALRAVYEAAQVTPLOKMEKLSRLDNYLVKREDROPVHS 60
 DB 1 MAVSQPLASAPCCAEYLRALRAVYEAAQVTPLOKMEKLSRVGTVLKRDRPVHS 60
 QY 61 FKRGAAYAMAGLTTEOKAHGVTASAGNHAQVAFSSARLGVKALIMPTATADIKVA 120
 DB 61 FKRGAAYAMISLTTEOKACGVTTASAGNHAQVAFSSARLGVKALIMPTATADIKVA 120
 QY 121 VRGFGSEVLLHGANFDEAKAKAIEISQOQGFVWPFPDHPVIAAGGTTALIELLODAH 180
 DB 121 VRAFGSEVLLHGANFDEAKAKAIALAQEGYTFVPPFDHPVIAAGGTTALIELLODAH 180
 QY 181 DRFVAVVGGGGLAAGVAVLIKOLMPQIKVIAVEASACIKALADGHPVDLPVGLFAE 240
 DB 181 DRFVAVVGGGGLAAGVAVLIKOLMPQIKVIGVEASACIKALADGHPVDLPVGLFAE 240
 QY 241 GVAVKRIGDEPFLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGKKYI 300
 DB 241 GVAVKRIGDEPFLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGKKYI 300
 QY 301 ALANRIGERLAHLISGANVFHGLRYVSERCELGOREALLAVTIPEKGSFLKFCOLLG 360
 DB 301 QQHNIGERLAHLISGANVFHGLRYVSERCELGOREALLAVTIPEKGSFLKFCOLLG 360
 QY 361 GRSVTEFNRYFAAKNACTIVGRLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVR 420
 DB 361 GRSVTEFNRYFAAENACTIVGRLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVR 420
 QY 421 YWVGGRPSHPLQRIYSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPE 480
 DB 421 YWVGGRPSHPLQRIYSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPE 480
 QY 481 XGDHEPDPETRLNELGYDCHDETNNPAFRFFLAG 514
 DB 481 LSATPEQFERLAALGYCHDETNDNPAFRFFLAG 514

RESULT 6
 Q8DDG2 PRELIMINARY; PRT; 509 AA.
 AC Q8DDG2;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Threonine dehydratase.
 GN VV11028.

OS *Vibrio vulnificus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxId=672;
 RN (1)
 RC SEQUENCE FROM N.A.
 RC STRAIN=CMC6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMC6.";
 RL Submitted (DEC-2002) to the EMBL/Genbank/DBD databases.
 DR EMBL; AE016800; AAO09516.1; -.
 KM Complete proteome.
 SQ SEQUENCE 509 AA; 55989 MW; BA29330A31822994 CRC64;

Query Match 71.7%; Score 1888.5; DB 16; Length 509;
 Best Local Similarity 70.7%; Pred. No. 2.1e-123;
 Matches 355; Conservative 68; Mismatches 78; Indels 1; Gaps 1;

QY 13 GAETLRALVRAVYEAAQVTPLOKMEKLSRLDNYLVKREDROPVHSFKLAGAYAMAG 72
 DB 8 GADYLRQILIRAVYEAAQVTPLOKMEKLSRLDNYLVKREDROPVHSFKLAGAYAMAG 67
 QY 73 LTEOKAHGVTASAGNHAQVAFSSARLGVKALIMPTATADIKVAVRFGSEVLLHG 132
 DB 68 LSOAQKDGAVITASAGNHAQVAFSSARLGVKALIMPTATADIKVAVRFGSEVLLHG 127
 QY 133 ANPDEAKAKAIEISQOQGFVWPFPDHPVIAAGGTTALIELLODAHIDRVAVPVGCGGL 192
 DB 128 SNPDEAKAKAIEISQOQGFVWPFPDHPVIAAGGTTALIELLODAHIDRVAVPVGCGGL 187
 QY 193 AAGVAVLIKOLMPQIKVIAVEASACIKALADGHPVDLPVGLFAEGVAVKRGDETF 252
 DB 188 AAGVAVLIKOLMPQIKVIAVEASACIKALADGHPVDLPVGLFAEGVAVKRGDETF 247
 QY 253 RLCOEYLDITVSDAICAMKDLFEDVRAVAPSGALALAGKKYIALANRIGERLAH 312
 DB 248 RLCOYHIDHYTVSSDEICAAVKDIFEDTRAIAPSGALALAGKKYAEKHLKGNLGT 307
 QY 313 IISGANVFHGLRYVSERCELGOREALLAVTIPEKGSFLKFCOLLGSRSTERNRYRA 372
 DB 308 VLSGANVFHGLRYVSERCELGOREALLAVTIPEKGAFFFCCHLIGRAVTEFNRYRN 367
 QY 373 DAKNACIFGVGLSGLEERKEIILOMLNDGYSVYDLSDDMAKLHVRWVGGRPSHPQ 432
 DB 368 DQSLANIFGVGLQNGEELDGIIRDLRGGYPPVVDLSDEDAKLHVRMIGKRSKPK 427
 QY 433 ERLYSEFPESPGAXLRFLNTLGTWYNISLFYRSHGTDYGRVLAPEXGDHE-PDEFTR 491
 DB 428 ERLYSEFPESPGALIKFLSTLGTWYNISLFYRNHGDYGRVLCGFELDESLSRFSAH 487
 QY 492 LNELGYDCHDETNNPAFRFFLA 513
 DB 488 LRELGYQCKDVTNDPSYRFFLS 509

RESULT 7
 Q9KWL1 PRELIMINARY; PRT; 510 AA.
 AC Q9KWL1;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 22, Last annotation update)
 DE Threonine dehydratase.
 GN VC0027.
 OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OX NCBI_TaxId=666;
 RN (1)
 RC SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Baas S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT cholerae";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004094; AAF93205.1; -
 DR HSSP; P04968; 1TDJ.
 DR TIGR; VC0027; -
 DR InterPro; IPR001926; B6 enzyme beta.
 DR InterPro; IPR000634; S/P dehydrtase.
 DR InterPro; IPR001721; ThnD_C.
 DR InterPro; IPR005787; Thn_dehydratase.
 DR Pfam; PF00291; PALP; 1.
 DR Pfam; PF00585; Thn dehydratase C; 2.
 DR TIGRFAMs; TIGR01124; llyA_2Cterm; 1.
 DR TIGR; PS00165; DEHYDRATASE_SER_THR; 1.
 KM Complete proteome.
 SQ SEQUENCE 510 AA; 56173 MW; 0690875549B38C25 CRC64;

Query Match 70.2%; Score 1849.5; DB 16; Length 510;
 Best Local Similarity 70.2%; Pred. No. 1,1e-120;
 Matches 354; Conservative 64; Mismatches 81; Indels 5; Gaps 2;

QY 13 GAETLRAVLRAVYEAQVTPLOKMEKLSRLDNLVILKREDRQVHSPKLRGAYAMAG 72
 DB 8 GAETLRAVLRAVYEAQVTPLOKMEKLSRLDNLVILKREDRQVHSPKLRGAYAMAG 67
 QY 73 LTBEGKANGVTASAGNNAQVAFSARLVKALVMTATADIVDVAVRGEGVLLHG 132
 DB 68 LTBEGKANGVTASAGNNAQVAFSARLVKALVMTATADIVDVAVRGEGVLLHG 127
 QY 133 ANPEAKAKATELSQOQFTWVPDPHPMVIAGQSTLALBELLODPAHIDRVFVPGGGGL 192
 DB 128 SNPEAKAKATELSQOQFTWVPDPHPMVIAGQSTLALBELLODPAHIDRVFVPGGGGL 187
 QY 193 AAGVAVLTKQMPQIKVIAVEADSAKLAALDAGHPVDLPVGLFAEGVAVKRIIGDET 252
 DB 188 AAGVAVLTKQMPQIKVIAVEADSAKLAALDAGHPVDLPVGLFAEGVAVKRIIGDET 247
 QY 253 RLCEYELDDITVDSDAICAMKDLFEDVRAVAESGALALAGMKYALANINIGERLAH 312
 DB 248 RLCEYELDDITVDSDAICAMKDLFEDVRAVAESGALALAGMKYALANINIGERLAH 307
 QY 313 ILTGANVPHGLRYVSERCGEORALLAVTIPREKSPFLKCOLLGGRSVTEPNYRFA 372
 DB 308 VLSGANVPHGLRYVSERCGEORALLAVTIPREKSPFLKCOLLGGRSVTEPNYRFA 367
 QY 373 DAKNACIFVGYRLSGLEERKEILQMLNDGYSVVDLSDDEMAKLVHVMYVGRPSHPLO 432
 DB 368 DDQANITFVGYRLSGLEERKEILQMLNDGYSVVDLSDDEMAKLVHVMYVGRPSHPLO 427
 QY 433 ERLVSFEPESPQAKLRLINTLGIYWNISLFTYRSHGTDYGRVLAFAFGXDHEP---FE 489
 DB 428 ERLVSFEPESPQAKLRLINTLGIYWNISLFTYRSHGTDYGRVLAFAFGXDHEP---FE 485
 QY 490 TRINELGYDCHDETNNPAPRFFLA 513
 DB 486 EHLVELGTRYKDETDNPAIRFFLA 509

RESULT 8
 OEB9EO PRELIMINARY; PRT; 545 AA.
 AC OEB9EO.
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Threonine dehydratase.

GN ILVA OR SC04344.
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Alteromonadaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MR-1;
 RX MEDLINE=22297686; PubMed=12368813;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Sehnadri R., Ward N., Methe B., Clayton R.A.,
 RA Meyer T., Tsaplin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
 RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
 RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
 RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
 RA Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.;
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT *Shewanella oneidensis*";
 RL Nat. Biotechnol. 20:1118-1123(2002).
 DR EMBL; AE015867; AAN57312.1; -
 DR TIGR; S04344; -
 KM Complete proteome.
 SQ SEQUENCE 545 AA; 58971 MW; 5CD1A85B4C95B3 CRC64;

Query Match 58.9%; Score 1550; DB 16; Length 545;
 Best Local Similarity 58.0%; Pred. No. 9.4e-100;
 Matches 304; Conservative 86; Mismatches 120; Indels 14; Gaps 4;

QY 2 ADSQPLSGAPEGAB-----YLRAVLRAVYEAQVTPLOKMEKLSRLDNLVILKRED 54
 DB 12 AESQPLSGAPEGAB-----YLRAVLRAVYEAQVTPLOKMEKLSRLDNLVILKRED 71
 QY 55 RQPVHFKLRGAYAMAGLTBEQAKHGYTTASAGNNAQVAFSARLVKALVMTATADIV 114
 DB 72 MQPVHFKLRGAYAMAGLTBEQAKHGYTTASAGNNAQVAFSARLVKALVMTATADIV 131
 QY 115 DIKDAVRGEGEVLILGANFDEAKAKATELSQOQFTWVPDPHPMVIAGQSTLALBEL 174
 DB 132 DIKDAVRGEGEVLILGANFDEAKAKATELSQOQFTWVPDPHPMVIAGQSTLALBEL 191
 QY 175 QODAHLDREVFPVGGGGLAGVAVLTKQMPQIKVIAVEADSAKLAALDAGHPVDLP 234
 DB 192 QODAHLDREVFPVGGGGLAGVAVLTKQMPQIKVIAVEADSAKLAALDAGHPVDLP 251
 QY 235 VGLFAEGVAVKRIIGDETFRLCQEYLDITVDSDAICAMKDLFEDVRAVAESGALALA 294
 DB 252 VGLFAEGVAVKRIIGDETFRLCQEYLDITVDSDAICAMKDLFEDVRAVAESGALALA 311
 QY 295 GMKYIALH-----NIRGERLAHILSGANVPHGLRYVSERCGEORALLAVTIPREK 350
 DB 312 GLKRYVSTNATGESGREGKVAALISGANVPHGLRYVSERCGEORALLAVTIPREK 371
 QY 351 SFLKFCOLLGSRSTVEPNYRPAADAKNACIFVGYRLSGLEERKEILQMLNDGYSVVDL 410
 DB 372 SFLKFCOLLGSRSTVEPNYRPAADAKNACIFVGYRLSGLEERKEILQMLNDGYSVVDL 431
 QY 411 DDEMAKLVHVMYVGRPSHPLOERLYSFEPESSQAKLRLINTLGIYWNISLFTYRSHG 470
 DB 432 DDEMAKLVHVMYVGRPSHPLOERLYSFEPESSQAKLRLINTLGIYWNISLFTYRSHG 491
 QY 471 DYGRVLAFAE---XGDHEPDEFTRLNELGYDCHDETNNPAPRFFLA 512
 DB 492 DYGRVLAFAE---XGDHEPDEFTRLNELGYDCHDETNNPAPRFFLA 534

RESULT 9
 O91418 PRELIMINARY; PRT; 515 AA.
 AC O91418.
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

Threonine dehydratase, biosynthetic.
 DE ILV2 OR PA1326.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxId=287;
 RX STRAIN=ATCC 15692 / PA01;
 RC MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino G., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Mong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL: AE004562; AAC04715.1; -.
 DR HSSP: P04968; ITDJ.
 DR InterPro: IPR001926; B6 enzyme_beta.
 DR InterPro: IPR000634; S/T_dehydrtse.
 DR InterPro: IPR001721; ThrDh_C.
 DR InterPro: IPR005787; Thr_dehydratet.
 DR Pfam: PF00291; PALP; 1.
 DR Pfam: PF00585; Thr_dehydrat_C; 2.
 DR TIGRfam: TIGR01124; ilvA_2cterm; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
 DR Complete proteome.
 SQ SEQUENCE 515 AA; 55903 MW; D06F9C512C791819 CRC64;

Query Match 53.8%; Score 1415.5; DB 16; Length 515;
 Best Local Similarity 54.4%; Pred. No. 2.1e-90;
 Matches 279; Conservative 95; Mismatches 132; Indels 7; Gaps 3;

1 MADSCPLSGAPBEGAEYLRAVRAVVEAQAQTPLQKMEKLSRLDNVILVKEEDROPVHS 60
 6 LSAASKPL-----AGYVESILAPVYDVAVETPLQVAPQISQLNGRVLKRDLPVPS 60
 61 FKLKGAAYAMAGLTTEOKAHGVTTSAGNHAQGVAFSSARLGKALIMPTATADIKVDA 120
 61 FKLKGAAYVRAVRLSDQKARGVITTSAGNHAQGLALAAQGLGVRAYIVMPTTPELKVNG 120
 121 VRFQGEVILHGANPBEAKKATELSQOQGFVTPPPDHMPVIAAGGTLALELLOQ-DNH 179
 121 VARGGBALHGAFPDALHQAQLAEREGMTFVPPDDPDVIAQGQTVAMEILKROHSGR 180
 180 LDFVFPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPVGLFA 239
 181 LDAIFPVGGGSLIAGIAAVKHLRPDIRIVGPEPDSNCLQAALAAGERVVLGQVGLFA 240
 240 EGVAVKRIQDETRLCQEYLDIIITVDSDAICAMKDLFEVRAVAEPPGALALAGMKKY 299
 241 DGVAVAQIQGACNEVECKDHVEVITVGSDEICAIKDIYDTRSITTEPAGALAVAGIKKY 300
 300 IALHNIRGERLAILISGANVPHGLRYVSRCELGOREALLAVTIPEEGSLKFCQL 359
 301 VAERTEGQTLVAIDSGANINPRLRHVARALGOREALIAVTAERGGSKATCAAL 360
 360 GGRSVTEFNYRFPADAKNACIFGVRLSRGLEERKEILQMLNDGYSVLDSDDEMAKLV 419
 361 GRQITFEFNYRHSDDQAHILFVGVOQHPLDLSADLADLAGREGFPVLDLTDNEMAKLH 420
 420 RYVWGRPSHPLQERLYSEFPESPQAKLRFNLTLGTWNISLFYRSHGTGYGVLAAP 479
 421 RHVWGGHGTVEVRERLRFEEFPERPCALLNFDKLSRWNI SLFHYRNHGAAGRYLAGI 480
 480 EXGDHE-PDEPTNLNGYDCHDETNNPARFP 511
 481 QVDEERGELEALQAIQPYMEETHNPAYRLF 513

RESULT 10
 ID 09JUX5 PRELIMINARY; PRT; 508 AA.
 AC 09JUX5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Putative threonine dehydratase biosynthetic (EC 4.2.1.16).
 GN ILV2 OR NMA1096.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_TaxId=656599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parikhil J., Achtmann M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltham T., Hamilton N., Holtroyd S.,
 RA Jørgensen K., Leather S., Moulé S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.,
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis 22491."
 RL Nature 404:502-506(2000).
 DR EMBL: AL162755; CAB84359.1; -.
 DR HSSP: P04968; ITDJ.
 DR InterPro: IPR001926; B6 enzyme_beta.
 DR InterPro: IPR000634; S/T_dehydrtse.
 DR InterPro: IPR001721; ThrDh_C.
 DR InterPro: IPR005787; Thr_dehydratet.
 DR Pfam: PF00291; PALP; 1.
 DR Pfam: PF00585; Thr_dehydrat_C; 2.
 DR TIGRfam: TIGR01124; ilvA_2cterm; 1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
 DR Complete proteome.
 SQ SEQUENCE 508 AA; 55212 MW; DBA18AF686A9932E CRC64;

Query Match 53.6%; Score 1410.5; DB 16; Length 508;
 Best Local Similarity 55.6%; Pred. No. 4.6e-90;
 Matches 280; Conservative 85; Mismatches 132; Indels 7; Gaps 4;

14 AEYLRAVRAVRYEAQAQTPLQKMEKLSRLDNVILVKEEDROPVHSFKLRGAYAMAGL 73
 8 SNYLRIILASTYDVAVETPLPAPSLSVRLKNVILKREDLPVPSFRLRAGVAKMSGL 67
 74 TEEQRAHGVITTSAGNHAQGVAFSSARLGKALIMPTATADIKVDVARGFGEVILHGA 133
 68 PDALACGVITTSAGNHAQGVAFSSARLGKALIMPTATADIKVDVARGFGEVILHGA 127
 134 NFEDEKAKKATELSQOQGFVTPPPDHMPVIAAGGTLALELLOQDHLD---RVFPVGGG 190
 128 SYNDAYDVAMELAEGGLTYAPFDDPDVIAQGQTVGMEIVSQ--HPDTRAVFPPIGGG 185
 191 GLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPVGLFAEGVAVKRIQDE 250
 186 GLAAGVAVLIKVREIKVIGVQNTDSCMKQSVBAGEIVHLKDVGLPSDGAIVKVGRE 245
 251 TFRLCQEYLDIIITVDSDAICAMKDLFEVRAVAEPPGALALAGMKKYIALHNIRGERL 310
 246 TFRLCQELDEIIITVDTAVCAVADIFDTRSITTEPAGALALAGLAKVIAREGAENQTL 305
 311 AAILISGANVPHGLRYVSRCELGOREALLAVTIPEEGSLKFCQLLGGRSVTEFNYR 370
 306 IAVTSGANNPRLRHVSRSRLGSGNGEIVFVTLPEEGSLKFCQLNLTGNNTFEFNR 365
 371 PADAKNACIFGVRLSRGLEERKEILQMLNDGYSVLDSDDEMAKLVRYVWGRPSHP 430
 366 YGDDEKANHFGVLQ-AAAGQDLAVIGSRUDEGLNVDLTDDEIKAHIRYVWGRPTDV 424
 431 LOERLYSEFPESPQAKLRFNLTLGTWNISLFYRSHGTGYGVLAAP-EXGDHE-PDE 489

[illegible]

Dd	240	VPGGGGILAGVASTLKALKEGVRIYGEPPDSDMATYSLOAGEVRLDVTGIFPDGVAIV	299
Oy	245	KRIGETFERLQOEYLDIIITVSDSAICAMKDLFEDVAVAPSPSASALAGMKXYIALHN	304
Dd	300	KQVGAYTFDRLRRYVDWMVRVNTDEVCAIKOVFPDTRVAVLEPAGALSVAHGKKYAAVHG	359
Oy	305	IRGERLAHILSGANVPFHGLRVSRCELGEORRELLAVTTIPBEKGSTFKFCOLLGGRSV	364
Dd	360	LHDRTLVALTCGANINFDRLRHVARBERTEIGEOREAIIIAVTIIPERGAFLPEFTELISRAI	419
Oy	365	TEFNRFADKANACIFGVGRLSRGLEBKRKEILOMNDGSYSVVDSDDEMAKLHVRYWVG	424
Dd	420	TEFNRIYAPREDARLFVGVLQGP-GEROELLTLRGGYAVLDTLEBELAKVHRHWG	478
Oy	425	GRPSHPLOERLYSEFPESPESGAXLERFLTLTGTWNISLFHNSHTGDYGRVLAEPXGDH	484
Dd	479	GRAPAVNVERVYAFFPPERGALHDFLQLQJCEMNISLFHYNNHSAGRVLAGVAV---	535
Oy	485	EPD-----FETRRLNELGYDCHEDETNNPAPRFL	512
Dd	536	-PDAALTFRGDFLAGIGYPADHVTSNPAYRFL	567
<p style="text-align:center;">RESULT 13</p>			
ID	O916G0	PRELIMINARY;	PRT; 504 AA.
AC	O916G0;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Theonine dehydrataae, biosynthetic.		
GN	ILVA1 OR PA0331.		
OS	Pseudomonas aeruginosa.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
CC	Pseudomonadaceae; Pseudomonas.		
OX	NCBI_Taxid=287;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 15692 / PAOI;		
RX	MEDLINE=20437373; PubMed=10984043;		
RA	Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrenner P.,		
RA	Hickey M.V., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,		
RA	Gardner R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,		
RA	Brody L.A., Coulter S.N., Folger K.R., Kas A., Labdig K., Lim R.M.,		
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,		
RA	Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;		
RT	"Complete genome sequence of Pseudomonas aeruginosa PAOI, an		
RT	opportunistic pathogen."		
RL	Nature 406:959-964(2000).		
RL	EMBL; AE004471; AAC03720.1; -.		
DR	EMBL; AE004471; AAC03720.1; -.		
DR	HSSP; P04968; 1TDJ.		
DR	InterPro; IPR001926; B6 enzyme beta.		
DR	InterPro; IPR000634; S/T dehydrtse.		
DR	InterPro; IPR001721; ThxDh_C.		
DR	InterPro; IPR005787; Thr_dehydrtatet.		
DR	pfam; PF00291; PALP; 1.		
DR	pfam; PF00585; Thr dehydrat C; 2.		
DR	TIGRFAMS; TIGR01124; ilva 2Ctem; 1.		
DR	PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.		
KM	Complete proteome.		
SQ	SEQUENCE 504 AA; 55351 MW; 055CEPF43E5A1BD73 CRC64;		
<p>Query Match 51.4%; Score 1354; DB 16; Length 504; Best Local Similarity 52.6%; Pred. No. 3, 9e-86; Matches 263; Conservative 95; Mismatches 140; Indels 2; Gaps 2</p>			
Oy	15	EYLRAVLPAFYEAQAOTPLQGMKEKISSSLDVIIVKREDROPVHSFKLRGAYVMAGIT	74
Dd	4	QYVKKITLSRVYDVAVEITLPQPARQISERLGNQVILLKREDDLPVPSFKIRGAYNKVAQLT	63
Oy	75	EEOKAHGVITAASNGHAQVAASSARLVGYKALITWPTAFADIKNDAVRRFGGEVILLGHAN	134

D6	EEBKAAGVIAASAGNHAQSLALAAKRGIRAVIIMPTKTPEIKQAIVBAHGAQAVLHGDA	122
OY	135 FDEAKAVALIEISOOQGFTWVPFPHPMVIYAGCGLALELL-QODAHLDRIYPVPGGGCLA	193
D6	124 FFELATLAALKLVKEGKGTFFVHPYDDPTLTIGOGGVAMEILRPOGRIDALFVPGGGGLV	183
OY	194 AGVAVLVKOLMPOIKVIAVEABDSCAKALLDAGHPVDLPVRVGFAGEVAVKRIGDETFR	253
D6	184 AGTAAVVKYLEPFLKTVIGVEDBSNCLOAMMAAGERVVYLQGVGLFADGVAVAOIGQHTFD	243
OY	254 LCOEYLDITITVSDSAICAAMKDLFEEDRAVAESPGLALAGMKKYIALHNIRGERLAHI	313
D6	244 ICKOHDEVITVSIDEICAAMKOIYDTRSIITEPAGALAIVAIGKIYVERREARBOQLVAI	303
OY	314 LSGANVNPHGLRVYSERCEIGEOREALLANTIPBEKKSFLKFQCLLGSRSTENYFPAD	373
D6	304 DSGANVNPFDRLRHVAERAEELGERREALIYAIVTIPERPSPFAFCBAVGKROIITENNYRH	363
OY	374 AKNACTPVGARLSGLBERKEILLMLMDGGSVYDLSDDEMAKLHVVMYMGARSHPLOE	433
D6	364 GSEAHITFVGOTHPENDPRELVAVYLEKGFPVLDDLTDNLAKLHIHMNGHAVKXISDE	423
OY	434 RLVSFFEPESFGAXIRLFNTLGTWNISLPHYRSHTDYDGRVLAIFEXGDHEPD-FETRL	492
D6	424 MVFFEFFEPERGALFNFLTUKLGKWMNISMPHYRNHGAADRNVAVGLQVFERHLILPQTL	483
OY	493 NELGYDCHDETNPAPRFPL 512	
D6	484 EAIGPYWDETPANPAYOLF 503	
 RESULT 14 O8YPG2 PRELIMINARY; PRT; 503 AA.		
ID	O8YPG2	
AC	O8YPG2;	
DT	01-MAR-2002 (TREMBLrel. 20, Created)	
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
DT	01-OCT-2002 (TREMBLrel. 22, last annotation update)	
DE	Threonine dehydratase.	
GN	ALR4232.	
OS	Anabaena sp. (strain PCC 7120).	
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.	
OX	NCHI_TaxID=103690;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=21595285; PubMed=11759840;	
RA	Kaneke T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,	
RA	Matenabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,	
RA	Kishida Y., Kohara S., Matsumoto M., Matsuno A., Muraki A.,	
RA	Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yanada M.,	
RA	Yasuda M., Tabata S.;	
RT	"Complete genomic sequence of the filamentous nitrogen-fixing	
RT	cyanobacterium Anabaena sp. strain PCC 7120."	
RL	DNA Ref. 8:205-213(2001).	
SM	EMBL; AP003595; BAB75931.1; -	
DR	InterPro; IPRO01926; B6_enzyme_beta.	
DR	InterPro; IPRO00634; S/T_dehydrtse.	
DR	InterPro; IPRO01721; ThTdN_C.	
DR	InterPro; IPRO05787; Thr_dehydratel.	
DR	Pfam; PF00291; PALP; 1.	
DR	Pfam; PF00585; Thr_dehydrat_C_2.	
DR	TIGRFAMS; TIGR01124; liva_2Cterm; 1.	
DR	PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 503 AA; 56026 MW; D9F6FCB40480348 CRC64;	
 Query Match 50.1%; Score 1318.5; DB 16; Length 503; Best Local Similarity 50.2%; Pred. No. 1.2e-83; Matches 251; Conservative 106; Mismatches 140; Indels 3; Gaps 3;		
OY	15 EYLRVAVLAAPYEAQVPTLCMEKELSSRLDNVILVKKREDQPVHSFKLRGAYMMAGLT	74
D6	4 DIVYOILTARKYDVDAQESPLEYARNLSARLNKLLKREDMQS/FSPFLRGRAYKNQVNL	63

Qy	75	BEOKHAGVITAAAGNHAOCVAFFSSARILVYKALIVMPTAADIKVDVAVRGGEVLLHGAN	134
Dd	64	PDLLAQGVITASAGNHAOCVALGAKOLGTRAILIVMPTVTPQYKVDVAVKARGGEVLLHGT	123
Qy	135	FDEAKAKAIELEGOOGGFTWPPBPDHVMVIAOGGTTALLELOQ-DAMHDRVYVVGGGGLA	193
Dd	124	YDDAAVAVARQLEAEKGLFPIHPFPDHPVIAOGOTIMEILLRQOGPIHAFVIAIGGGIL	183
Qy	194	AGVANLILQOLMPOIKVIANEADDSACTKALDAGHVLDLPRVCLFABGAVAKRIGETPR	253
Dd	184	SGIAAYVRLRPEIKIIGVEPVADAMNOSLOAKGRVRLSOGVLFADGAVAVRVEGETER	243
Qy	254	LCOEYLDIDIIIVDSDAICAMKDLFEDYVAVAEPSSGALALAGMKKXIALHNIIGESLAIH	313
Dd	244	LCQEVDEIILVDTDTQCAIKDVFEDTRSLIEPACALAIAGKAVVBERQIQGLTVAV	303
Qy	314	LSGANVNHGLRYVSERCLEGEORELLAVTIPEEKSGFLTKFOQLIGRSVTEFNTRPAD	373
Dd	304	ACGAMMNDRLRFEVABERAFGERREAIIPAVTIPETGSRKKECECGRRTLTFENRIAD	363
Qy	374	AKNACIFGVRLSRGLSEERKEILLOMANDGYSVVDSDDEMAKLAHYRVYMGGSPSHLOE	433
Dd	364	EKIAIIFIGMOQ-QNRADIKIHAVETFAEGGFEILIDTDBELTGLIHRNVGGISPLAHNE	422
Qy	434	RLYSFEPESPAGALRLFTLITGYWNISLFHYRSHGTDYGRVLAAEKXGDHE-PDFETRL	492
Dd	423	LLYREFEPPERPALMKFVASMSPNWNIISMFHYRNNSDGRIVVGMQVPOEEMEWQAF	482
Qy	493	NEIGYDCHDETNNPAFRFL	512
Dd	483	DSLGIQYMWDESONPAKFL	502

RESULT 15	
Q8Y287	
ID Q8Y287	PRELIMINARY; PRT; 507 AA

DT 01-MAR-2002 (TREMblrel. 20. Created)
 DT 01-MAR-2002 (TREMblrel. 20. Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22. Last annotation update)
 DE Probable threonine dehydratase (Threonine deaminase) transmembrane
 DE protein (EC 4.2.1.16).
 GN ILVA OR RSC0449 OR RS04453.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 CX NCBI_taxid=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM1100;
 RC MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gonzy J., Mangnot S.,
 RA Ariat M., Billault A., Brotier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunne S., Demange N.,
 RA Gaepin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Rappaport J., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weisenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL, AL646059, CAD13977.1, -.
 DR InterPro, IPR001926; B6 enzyme_beta.
 DR InterPro, IPR000634; S/T dehydratase.
 DR InterPro, IPR001721, TrnDh_C.
 DR InterPro, IPR005787; Trn_dehydratase.
 DR Pfam, PF00291, PALP; 1. _dehydratase.
 DR Pfam, PF00585; Thr dehydratase C: 2.
 DR TIGRfam, TIGR01124; ilva_2Cterm; 1.
 DR PROSITE, PS00165; DEHYDRATASE_SER_THR; 1.
 SQ Lysae, Complete proteome.
 SEQUENCE 507 AA; 55666 MW; 1C7A0467BC5F644 CRC64;

Query Match 49.7%; Score 1307.5; DB 16; Length 507;

Best Local Similarity 51.8%; Pred. No. 7e-83;
Matches 263; Conservative 90; Mismatches 140; Indels 15; Gaps 6;

[illegible]

Search completed: December 18, 2003, 15:29:42
Job time : 42 secs

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